HUMAN TELOMERASE

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG      60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu      20

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG     120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln      40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG     180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp      60

GACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTG     240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu      80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC     300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly     100

TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGC     360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg     120

AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG     420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu     140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG     480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal     160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT     540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla     180

GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA     600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu     200

CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT     660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly     220

GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT     720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg     240
```

FIG. 1A

```
GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGC    780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly    260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA    840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu    280

GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC    900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly    300

CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT    960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro    320

TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG   1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln    340

CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC   1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu    360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC   1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro    380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC   1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis    400

GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC   1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr    420

CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG   1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu    440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG   1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln    460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC   1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer    480

AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT   1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis    500
```

FIG. 1B

```
GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG   1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu    520

CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC   1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle    540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC   1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe    560

TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC   1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal    580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG   1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu    600

CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA   1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg    620

CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG   1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal    640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA   1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla    660

CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTG   2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal    680

CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG   2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln    700

GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC   2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle    720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC   2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys    740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG   2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys    760
```

FIG. 1C

```
AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG   2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu    780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG   2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu    800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC   2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle    820

AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG   2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu    840

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC   2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp    860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG   2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla    880

AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG   2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu    900

CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT   2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal    920

CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG   2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu    940

GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC   2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe    960

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG   2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu    980

AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC   3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn   1000

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA   3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro   1020
```

FIG. 1D

```
TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC   3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls   1040

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC   3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly   1060

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC   3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu   1080

AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG   3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln   1100

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC   3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn   1120

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACtgatggccacccgcccacagccag   3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp                           1132

Gccgagagcagacaccagcagccctgtcacgccgggctctacgtcccagggagggagggg   3480
Cggcccacacccaggcccgcaccgctgggagtctgaggcctgagtgagtgtttggccgag   3540
gcctgcatgtccggctgaaggctgagtgtccggctgaggcctgagcgagtgtccagccaa   3600
gggctgagtgtccagcacacctgccgtcttcacttccccacaggctggcgctcggctcca   3660
ccccagggccagcttttcctcaccaggagcccggcttccactccccacataggaatagtc   3720
catccccagattcgccattgttcacccctcgccctgccctcctttgccttccacccccac   3780
catccaggtggagaccctgagaaggaccctgggagctctgggaatttggagtgaccaaag   3840
gtgtgccctgtacacaggcgaggaccctgcacctggatgggggtccctgtgggtcaaatt   3900
ggggggaggtgctgtgggagtaaaatactgaatatatgagttttcagttttgaaaaaaa   3960
aaaa                                                           3964
```

FIG. 1E

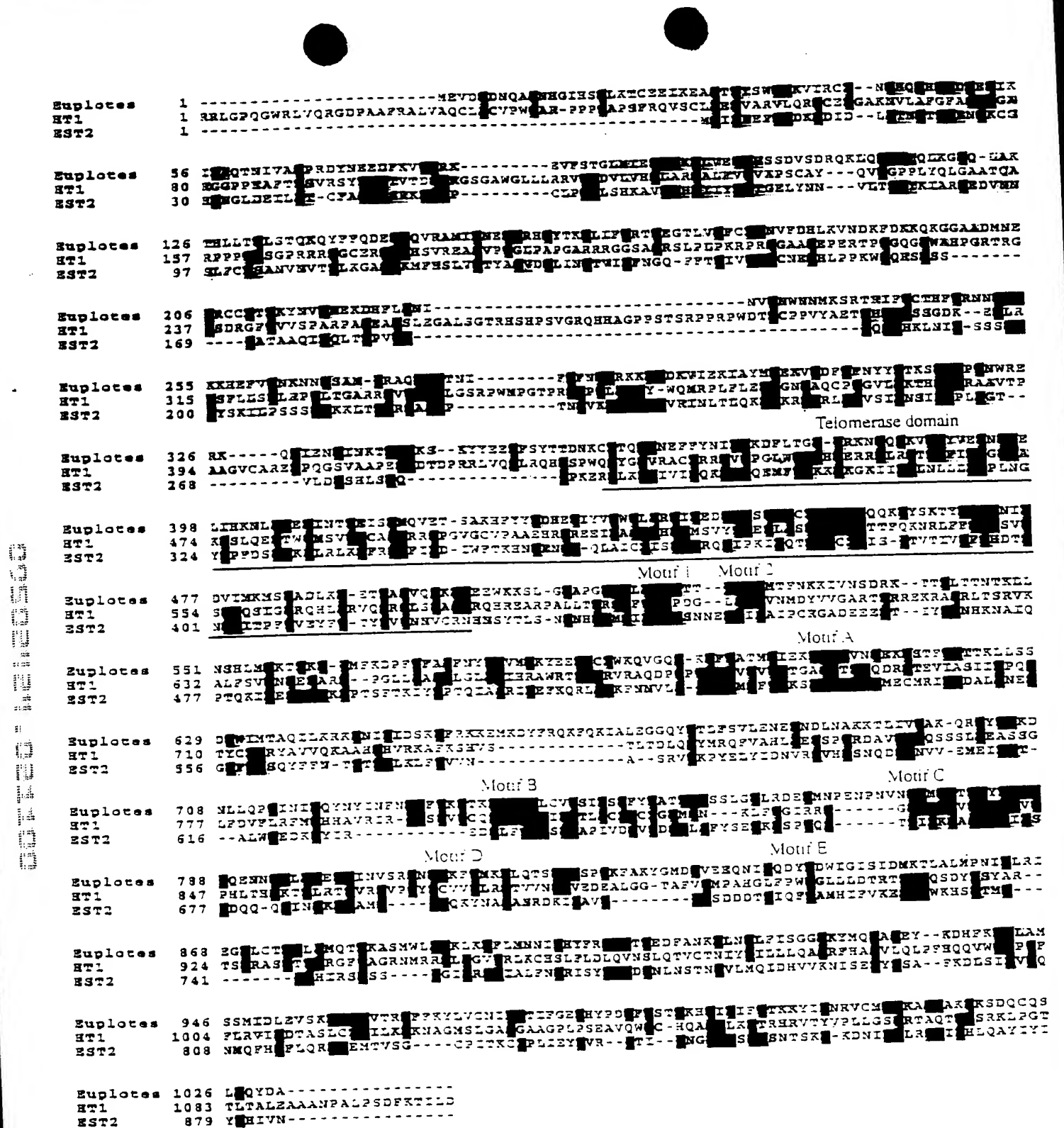

Euplotes
HT1
EST2
Telomerase domain
Motif 1
Motif 2
Motif A
Motif B
Motif C
Motif D
Motif E

FIG. 2

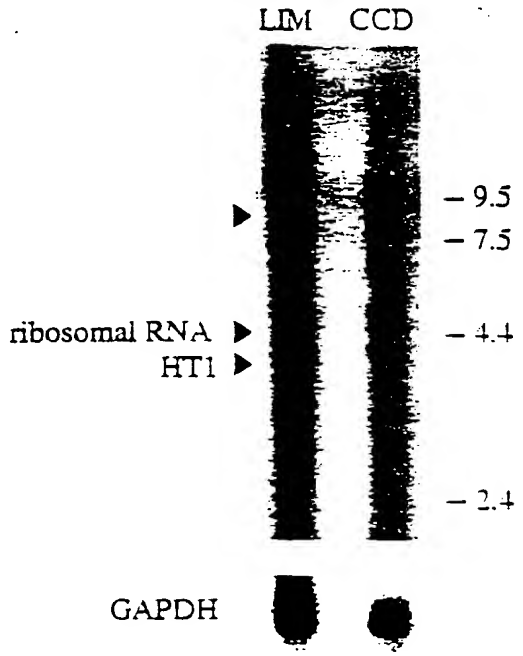


FIG. 3

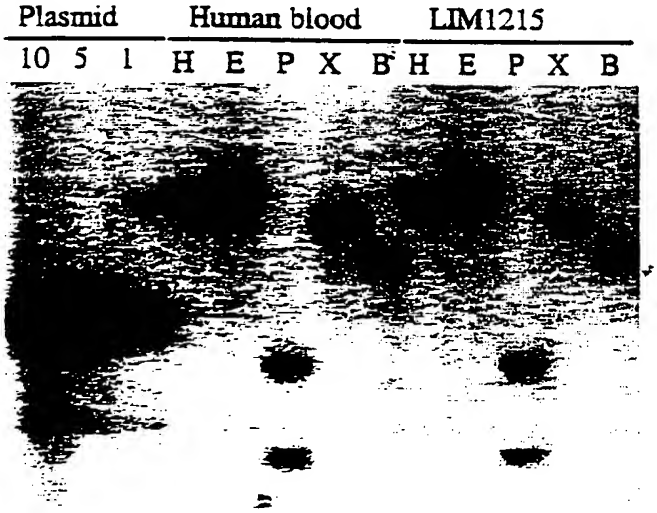


FIG. 4

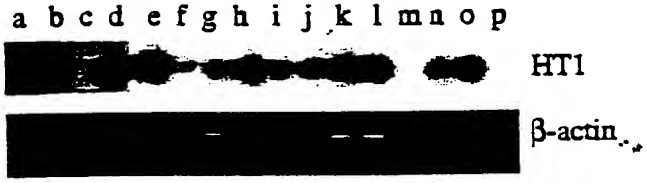
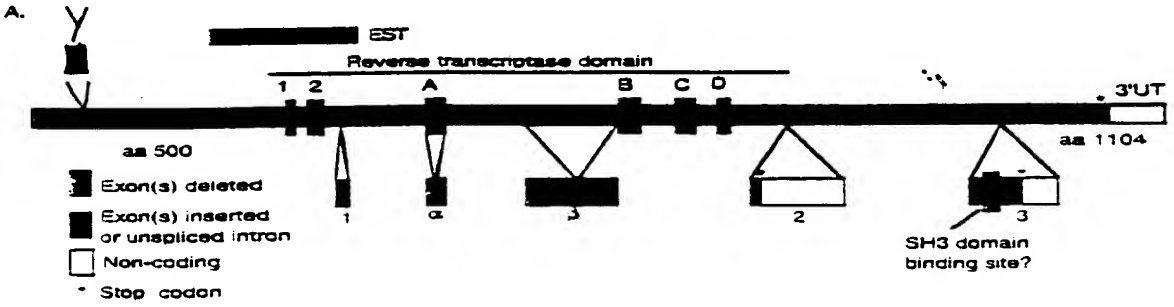


FIG. 5

FIG. 6

A.



B.

Variants:	1	α	B	2	3
RT-PCR product	ND	+	+	ND	+ & -
PCR from LIM1215 lib.	-	+	-	+	ND
RT-PCR product	ND	-	+	ND	+
53.2 cDNA	-	-	-	-	ND

FIG. 7A and 7B

C

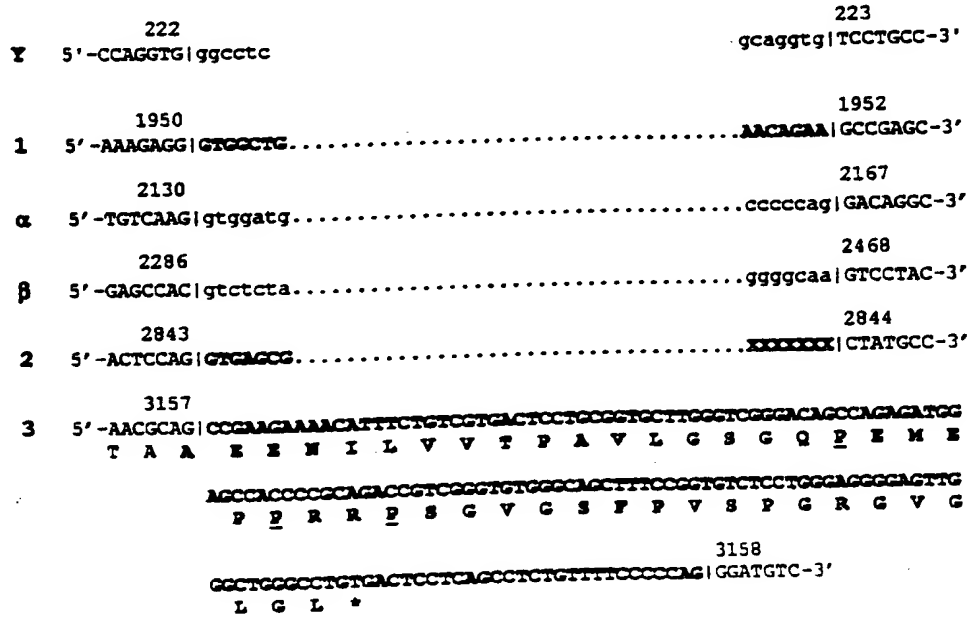

222
Y 5'-CCAGGTG|ggcctc
223
gcaggtg|TCCTGCC-3'
1950
1 5'-AAAGAGG|GTGGCTG
1952
|GCCGAGC-3'
2130
α 5'-TGTCAAG|gtggatg
2167
|GACAGGC-3'
2286
β 5'-GAGCCAC|gtctcta
2468
|GTCCTAC-3'
2843
2 5'-ACTCCAG|GTGAGCG
2844
|CTATGCC-3'
3157
3 5'-AACGCAG|
T A A E E N I L V V T P A V L G S G Q P E M E
P P R R P S G V G S F P V S P G R G V G
3158
L G L *
|GGATGTC-3'

FIG. 7C

FIG. 8

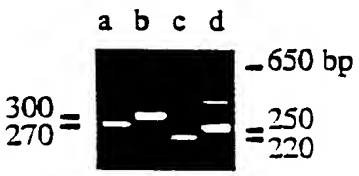


FIG. 9

sequence "γ" 104-105 bases

```
GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAG
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln
 AlaSerProGlySerAlaSerGlyTrpGly * GlyArgProGlyGlyThrSer
  ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg
 AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly
  ThrCysGlyGluGlnArgArgArgLeuArgAlaLeuProProGlnVal
```

sequence "1" 38 bases

```
GTGGCTGTGCTTTGGTTTAAGTTCCTTTTTAACCAGAA
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys
```

sequence "α" 36 bases

```
GTGGATGTGACGGGCGCGTACGACACCATCCCCCAG
ValAspValThrGlyAlaTyrAspThrIleProGln
```

sequence "β" 182 bases

```
GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTG
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeu

AATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCAC
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis

GCCGTGCGCATCAGGGGCAA
AlaValArgIleArgGlyLys
```

partial sequence "2" unknown length

```
GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAG
 Ter

GGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGT
CAGATGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTG
TGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA...
```

sequence "3" 159 bases

```
 CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTCGGGACAGCCAGAG
AlaGluGluAsnIleSerValValThrProAlaValLeuGlySerGlyGlnProGlu

ATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGG
MetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg

GGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
GlyValGlyLeuGlyLeu *
```

FIG. 10A

sequence "X" unknown length

...GACAGTCACCAGGGGGGTTGACCGCCGGACTGGGCGTCCCCAGGGTTGACTATAGGA
CCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGGCATGG
GTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCT
CACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTGG
CTGAGCAAGCCTCCTGAGGGGCTCTCTATTG

partial sequence of genomic intron (approximately 2.7 kb)

GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAAGTGCGTTTGAGCCCCACATT
TGGTATCAGCTTAGATGAAGGGCCCGGAGGAGGGGCCACGGGACACAGCCAGGGCCAT
GGCACGGCGCCCACCCATTTGTGCGCACAGTGAGGTGGCCGAGGTGCCGGTGCCTCCA
GAAAAGCAGCGTGGGGGTGTAGGGGGAGCTCCTGGGGCAGGGAC....

FIG. 10B

N-terminal truncated telomerase

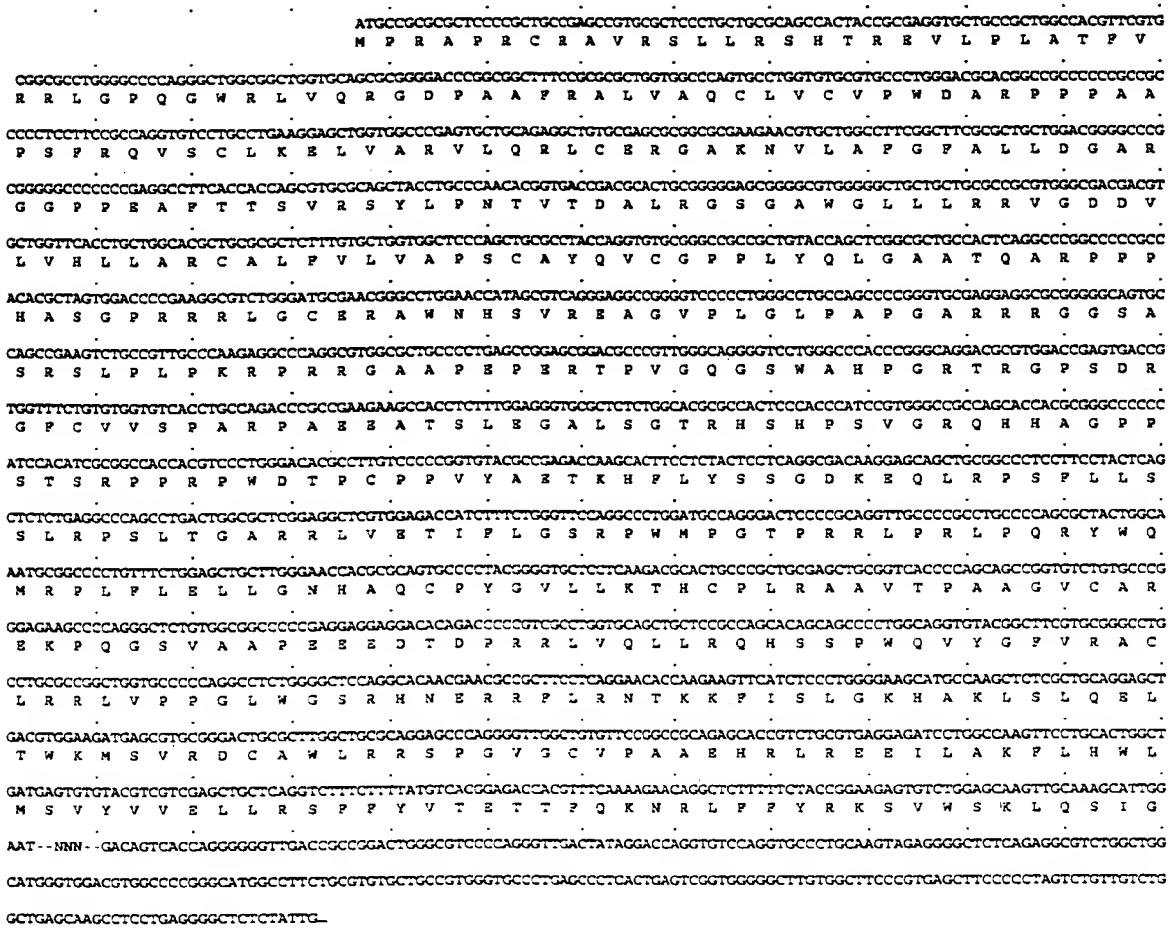


FIG. 11A

Truncated protein 1

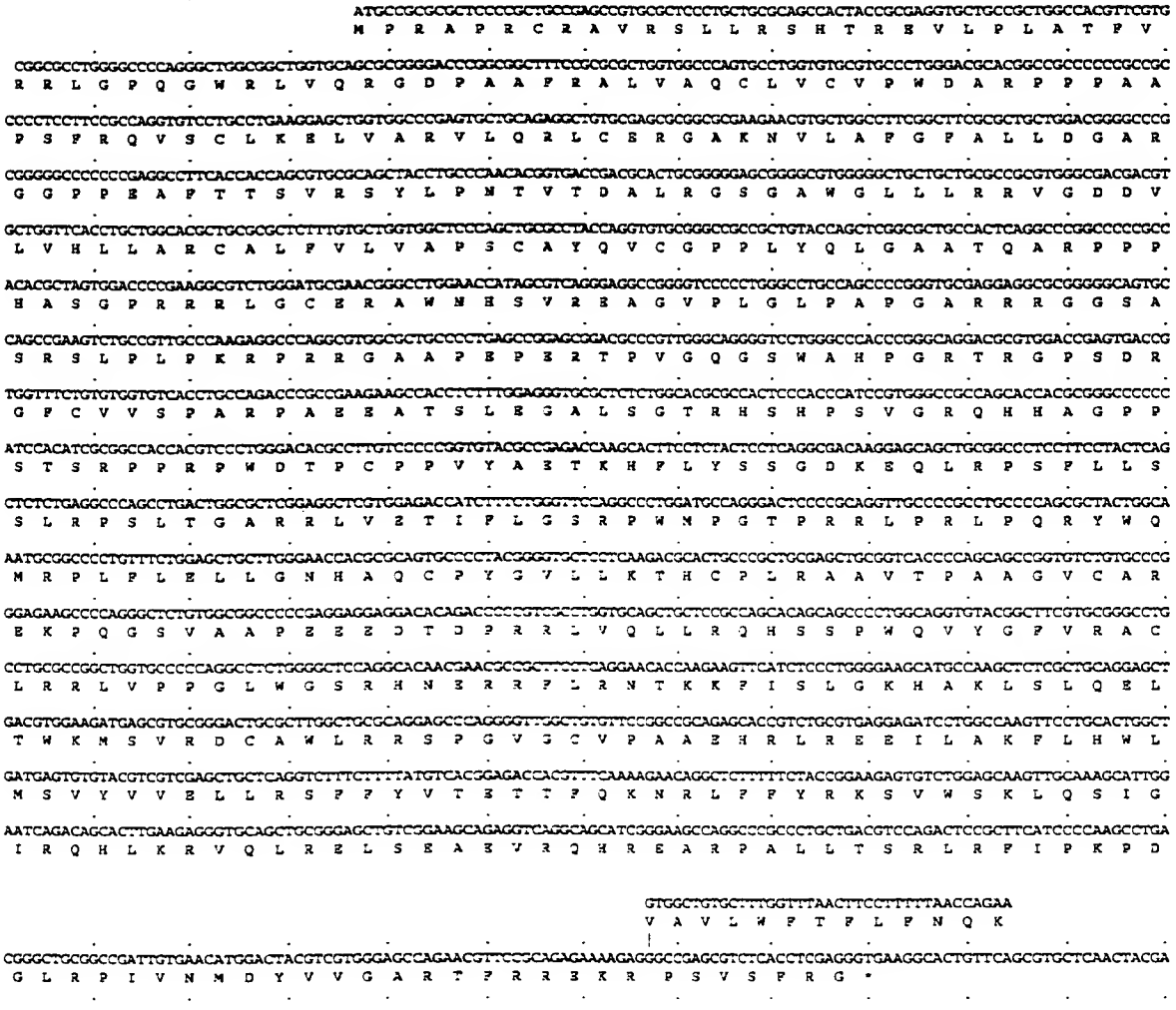


FIG. 11B

Truncated protein 2

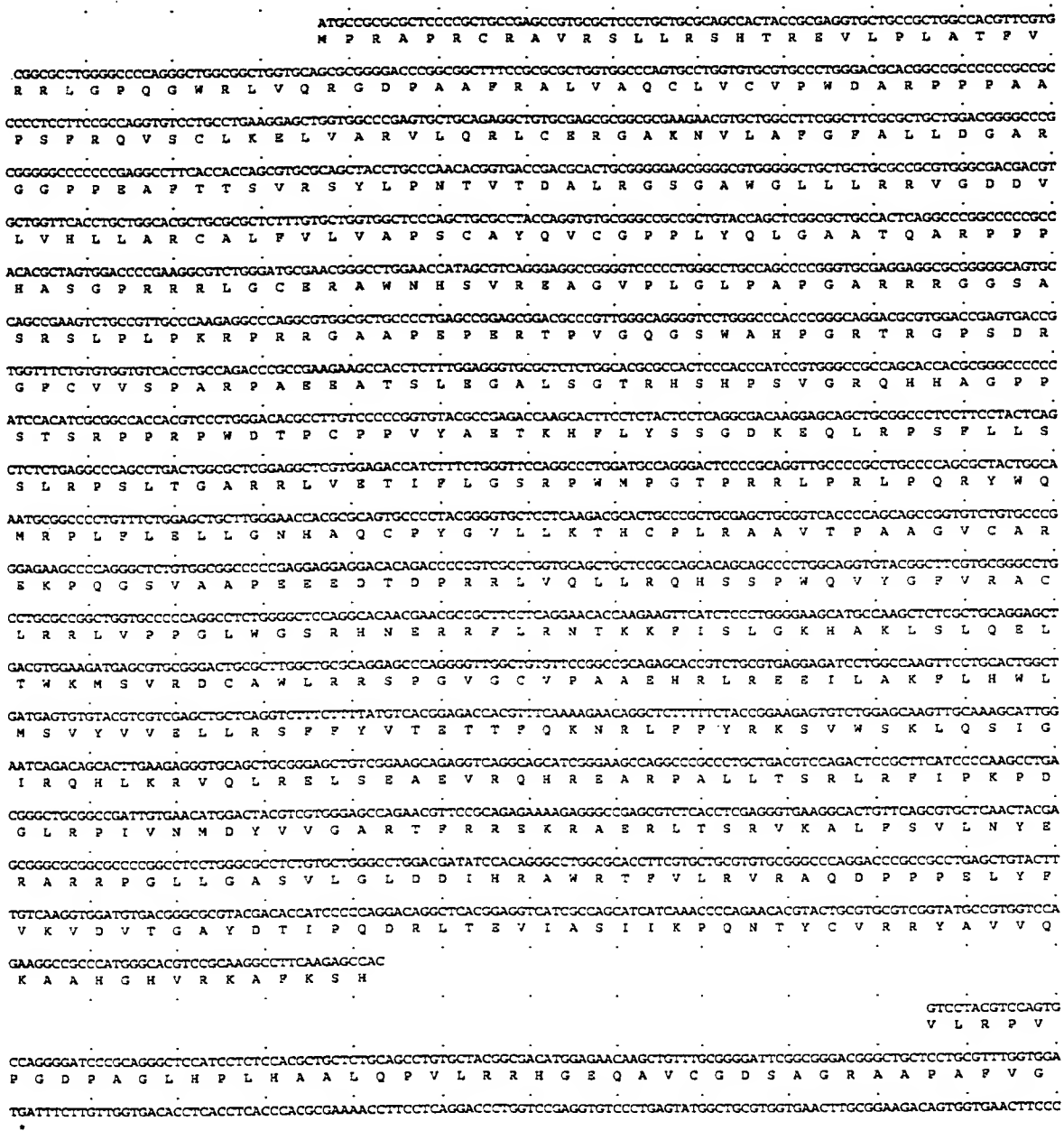


FIG. 11C

Reference protein

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG     60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu     20

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG    120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln     40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG    180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp     60

GACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTG    240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu     80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC    300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly    100

TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCCGAGGCCTTCACCACCAGCGTGCGC    360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg    120

AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG    420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu    140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG    480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal    160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT    540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla    180

GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA    600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu    200

CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT    660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly    220

GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT    720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg    240

GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGC    780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly    260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA    840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu    280

GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC    900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly    300

CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT    960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro    320

TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG   1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln    340

CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC   1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu    360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC   1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro    380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC   1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis    400

GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC   1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr    420
```

FIG. 11D

```
CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG   1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu     440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG   1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln     460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC   1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer     480

AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT   1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis     500

GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG   1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu     520

CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC   1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle     540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC   1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe     560

TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC   1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal     580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG   1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu     600

CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA   1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg     620

CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG   1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal     640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA   1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla     660

CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTG   2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal     680

CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG   2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln     700

GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC   2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle     720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC   2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys     740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG   2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys     760

AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG   2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu     780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG   2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu     800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC   2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle     820

AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG   2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu     840

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC   2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp     860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG   2640
```

FIG. 11E

```
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla      880
          .         .         .         .         .         .

AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG    2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu      900
          .         .         .         .         .         .

CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT    2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal      920
          .         .         .         .         .         .

CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG    2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu      940
          .         .         .         .         .         .

GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC    2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe      960
          .         .         .         .         .         .

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG    2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu      980
          .         .         .         .         .         .

AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC    3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn     1000
          .         .         .         .         .         .

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA    3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro     1020
          .         .         .         .         .         .

TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC    3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls     1040
          .         .         .         .         .         .

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC    3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly     1060
          .         .         .         .         .         .

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC    3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu     1080
          .         .         .         .         .         .

AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG    3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln     1100
          .         .         .         .         .         .

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC    3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn     1120
          .         .         .

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC                             3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp                             1132
```

FIG. 11F

Truncated protein 3

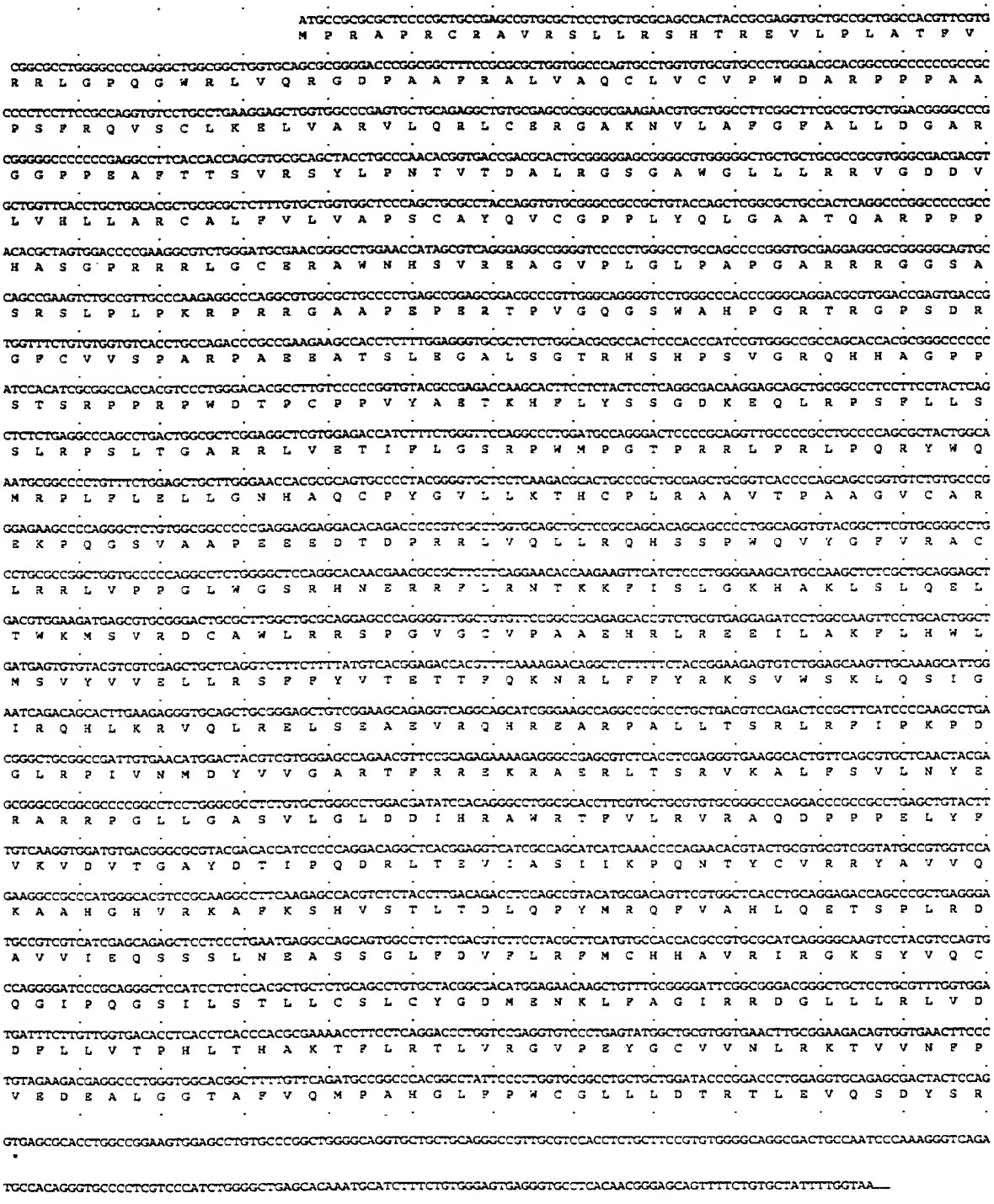


FIG. 11G

Altered C-terminus protein

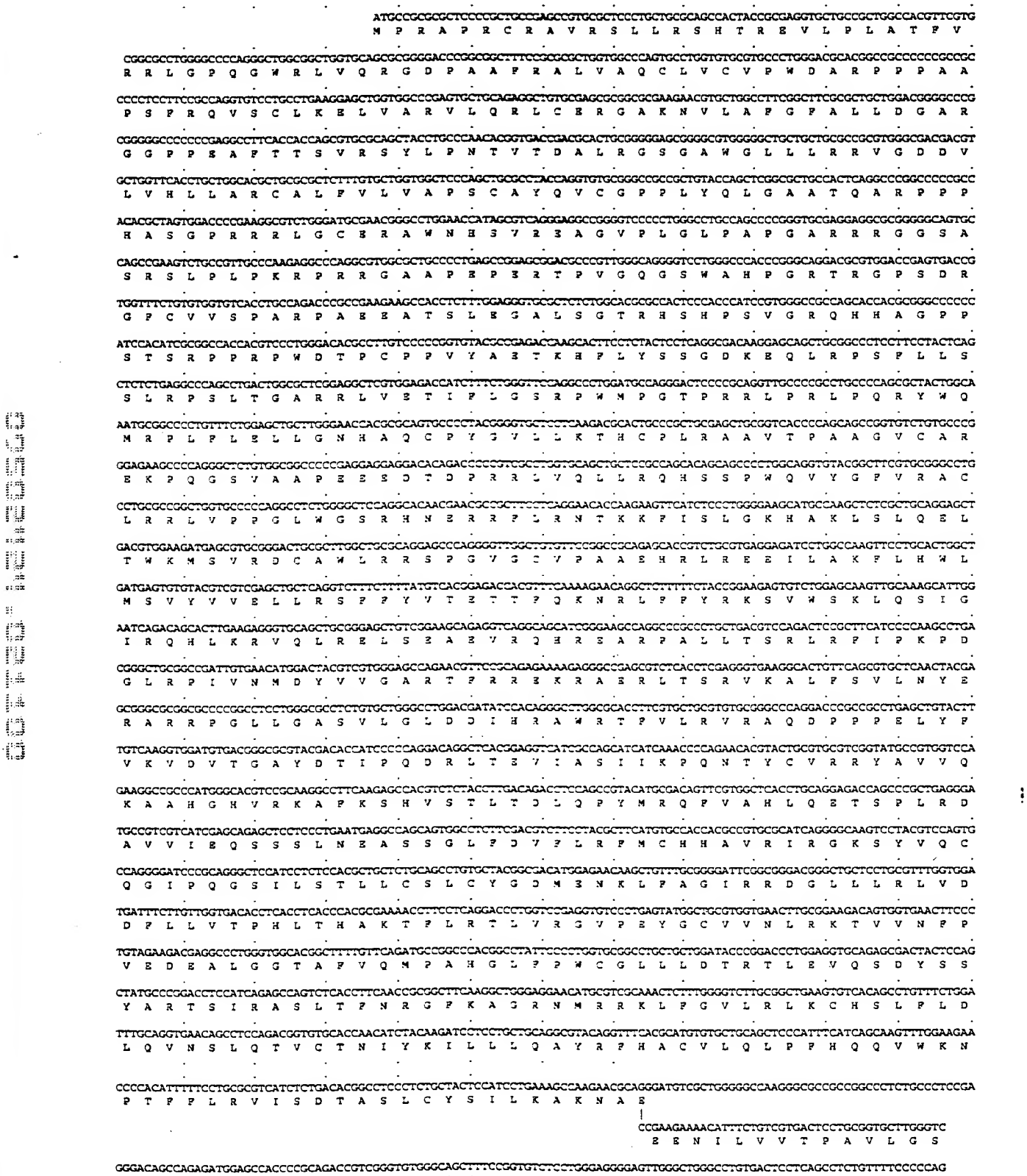


FIG. 11H

[redacted] Protein that lacks motif [redacted]

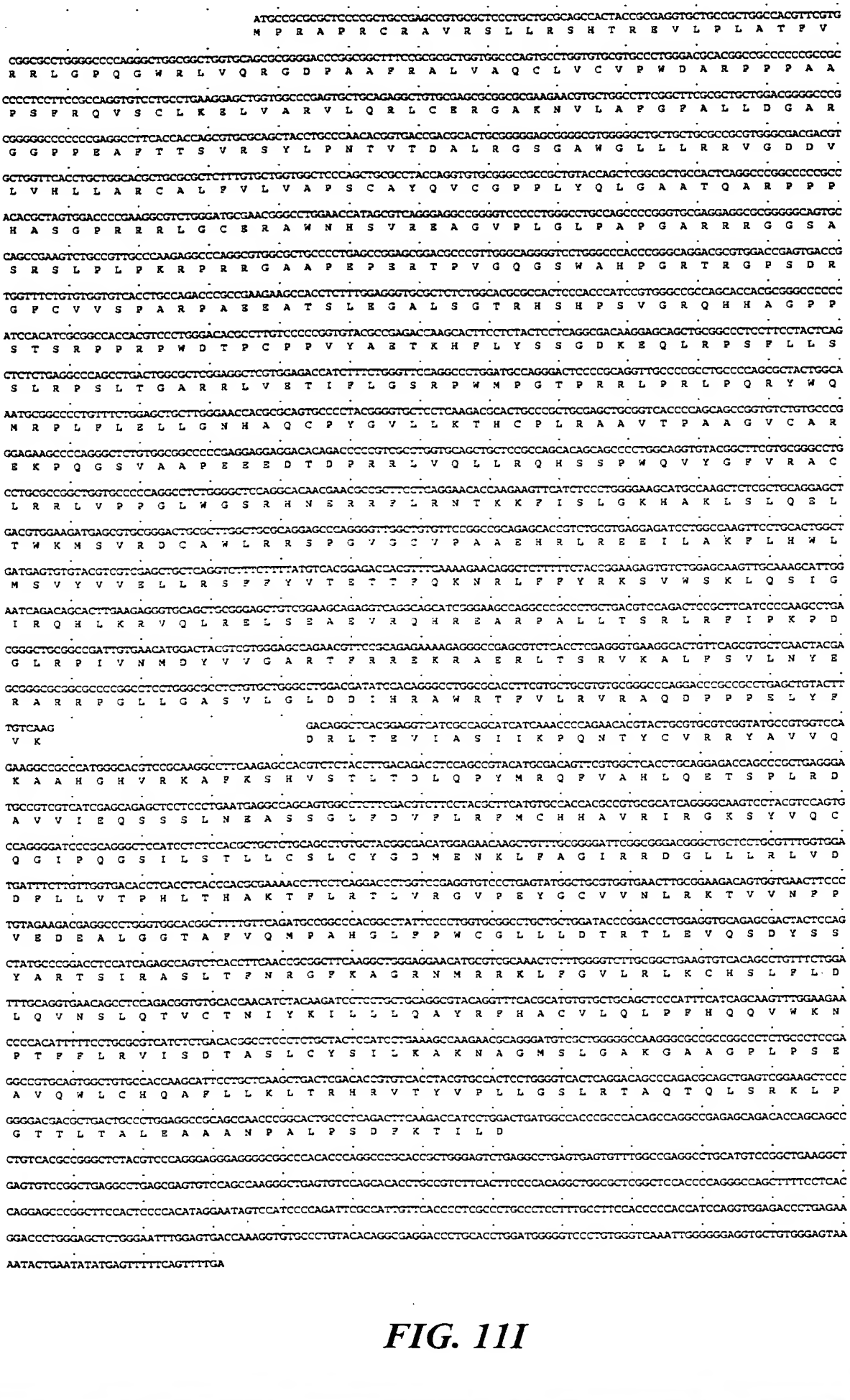


FIG. 11I

Tr[redacted]ated protein that lacks [redacted]if A

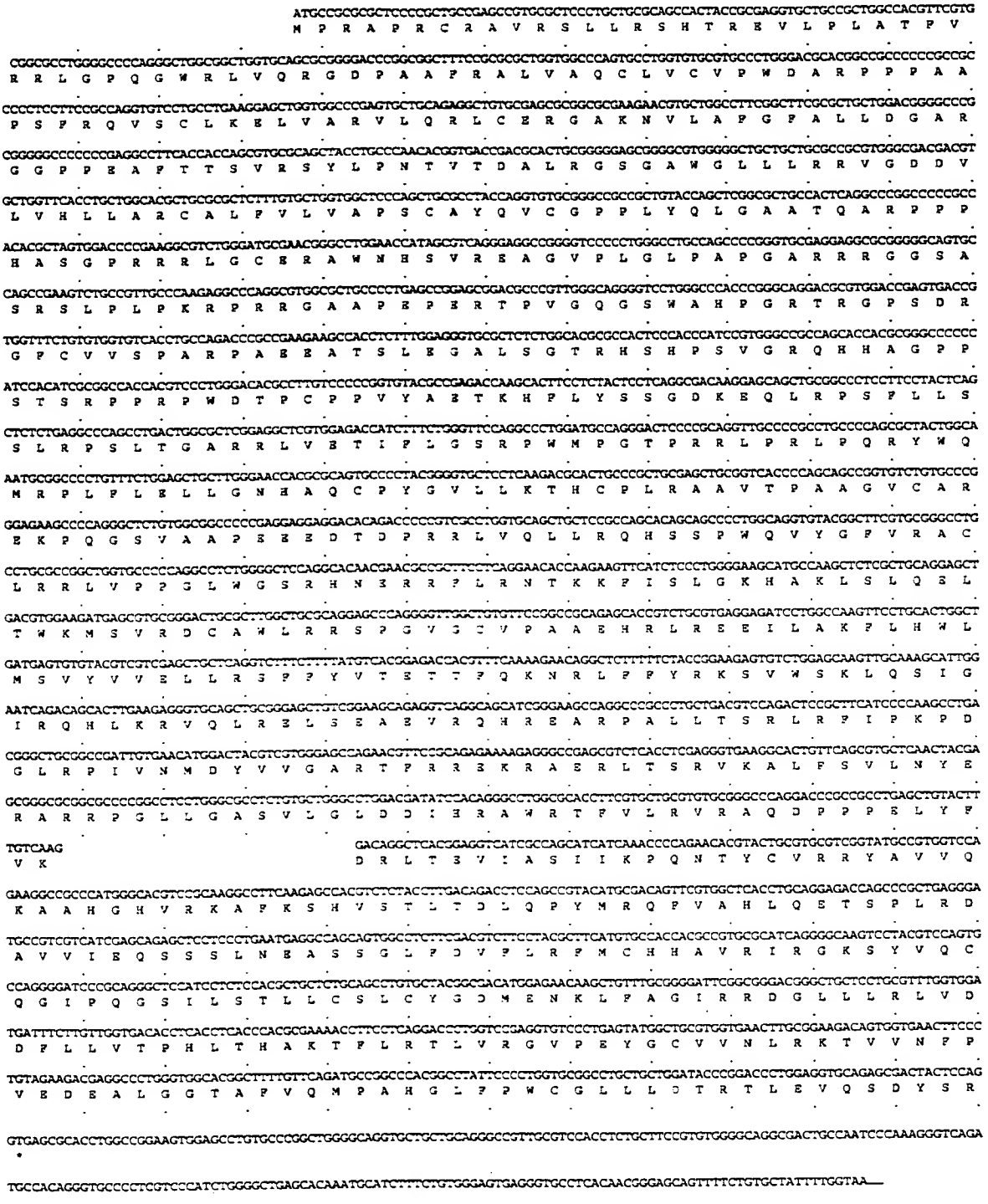


FIG. 11J

La[redacted]s motif A and altered C-t[redacted]inus

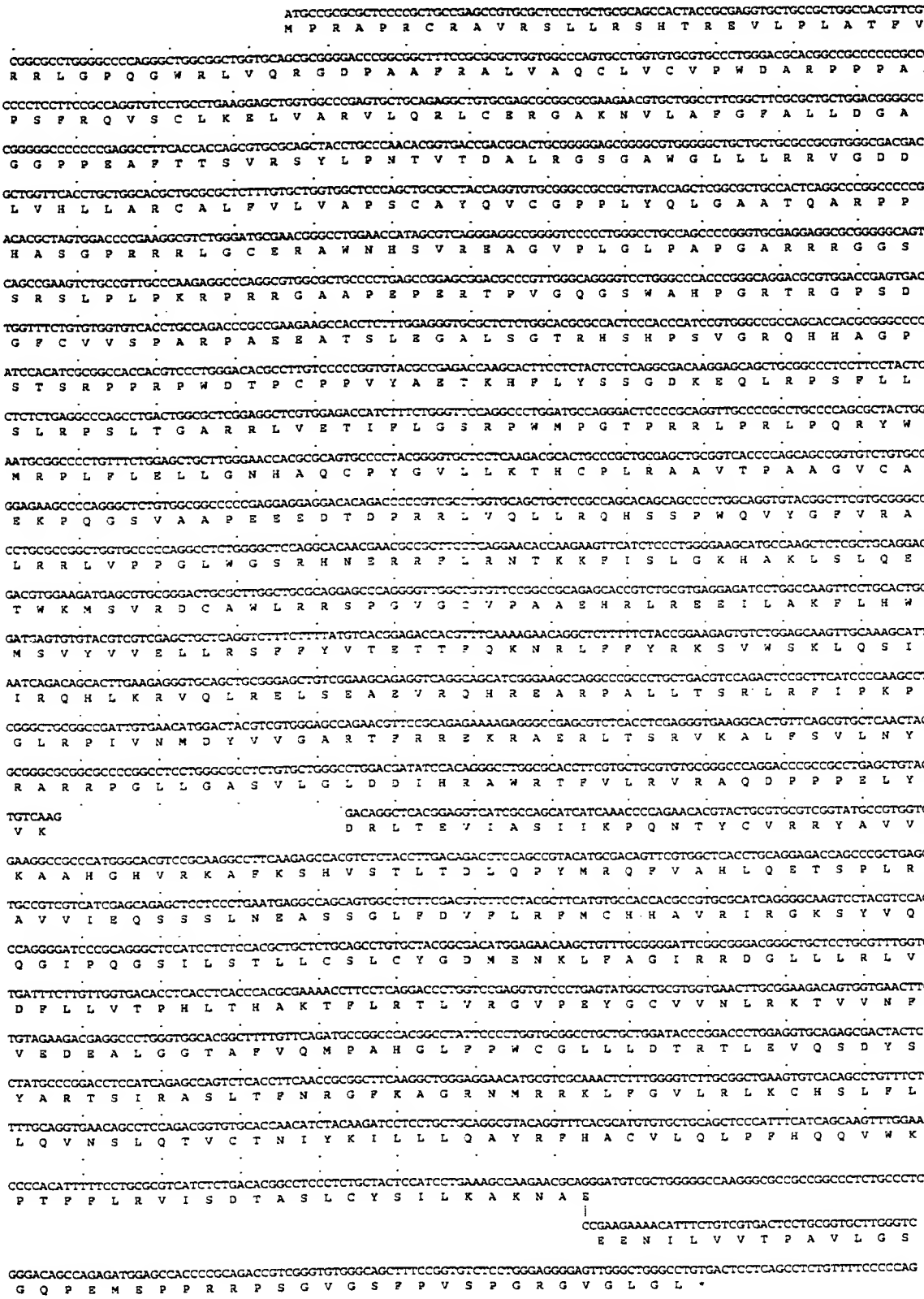
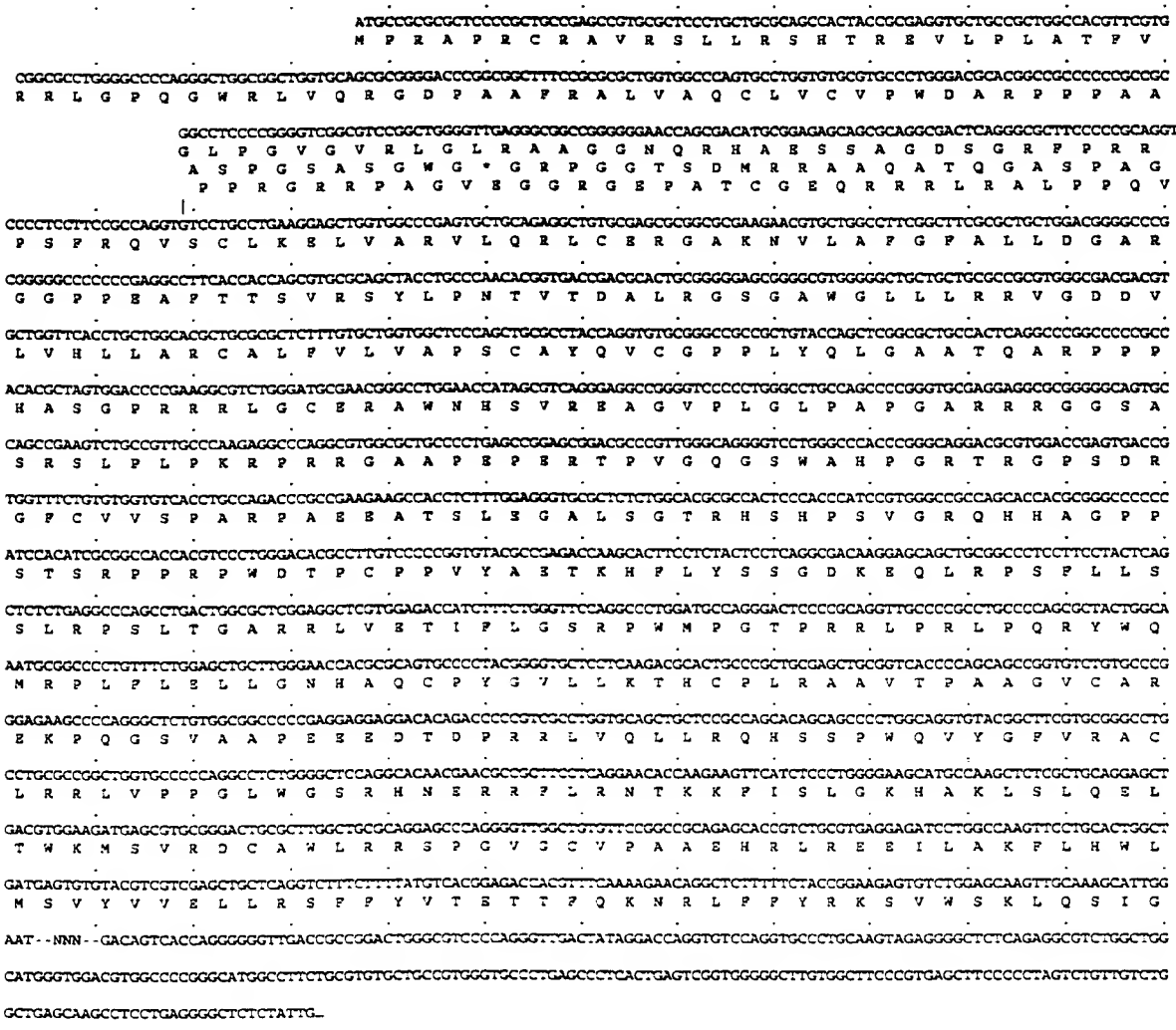


FIG. 11K

N-t[redacted]inal truncated telomerase [redacted]ver. 2)



ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H T R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCTCGTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AAT--NNN--GACAGTCACCAGGGGGGTTGACCGCCGGACTGGGCGTCCCCAGGGTTGACTATAGGACCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGG

CATGGGTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTG

GCTGAGCAAGCCTCCTGAGGGGCTCTCTATTG

FIG. 11L

Truncated protein 1 (ver.

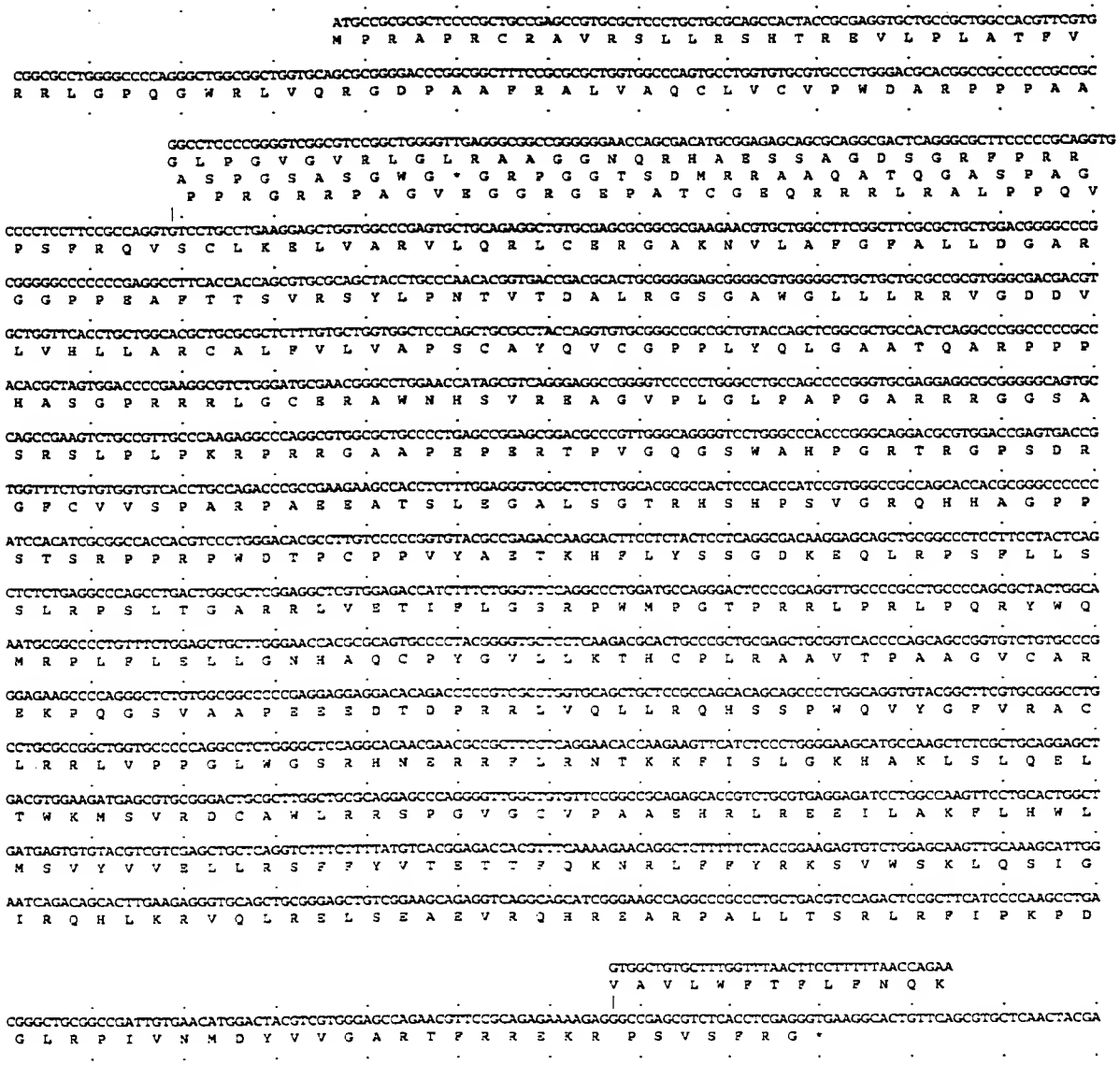


FIG. 11M

[redacted]uncated protein 2 (ver.[redacted]

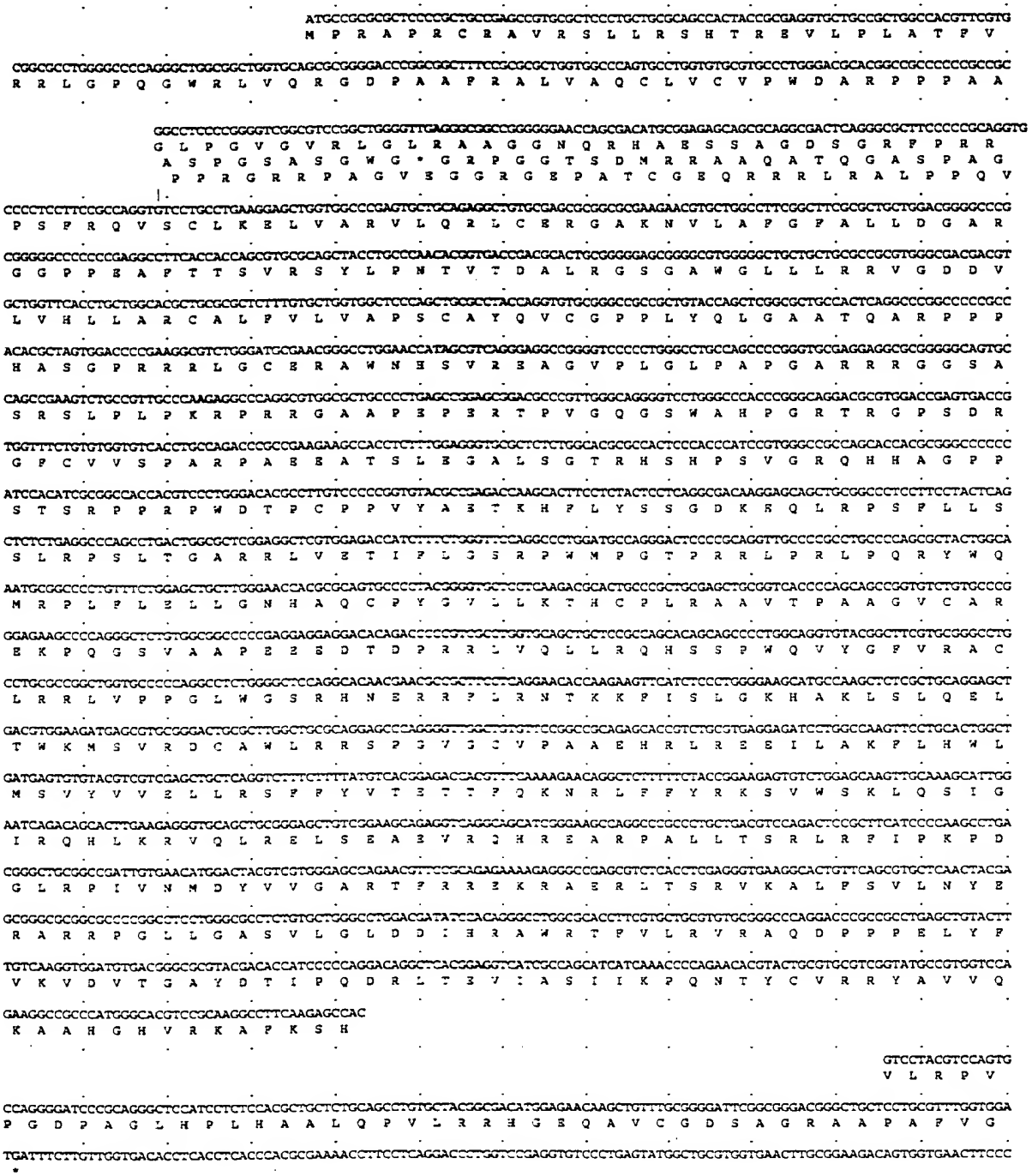


FIG. 11N

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG      60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu      20

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG     120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln      40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG     180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp      60

GACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTG
AspAlaArgProProProAlaAlaProSerPheArgGlnVal

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
 A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
  P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

TCCTGCCTGAAGGAGCTG     240
SerCysLeuLysGluLeu      80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC     300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly     100

TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCCGAGGCCTTCACCACCAGCGTGCGC     360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg     120

AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG     420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu     140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG     480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal     160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT     540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla     180

GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA     600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu     200

CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT     660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly     220

GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT     720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg     240

GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGC     780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly     260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA     840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu     280

GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC     900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly     300

CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT     960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro     320

TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG    1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln     340

CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC    1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu     360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC    1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro     380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC    1200
```

FIG. 110

```
ArgLeuProGlnArgTyrTrpGlnMet[redacted]roLeuPheLeuGluLeuLeuGlyAsnHis [redacted]

GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC  1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr   420

CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG  1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu   440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG  1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln   460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC  1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer   480

AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT  1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis   500

GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG  1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu   520

CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC  1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle   540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC  1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe   560

TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC  1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal   580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG  1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu   600

CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA  1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg   620

CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG  1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal   640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA  1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla   660

CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTG  2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal   680

CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG  2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln   700

GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC  2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle   720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC  2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys   740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG  2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys   760

AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG  2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu   780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG  2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu   800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC  2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle   820

AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG  2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu   840

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC  2580
```

FIG. 11P

```
LeuCysSerLeuCysTyrGlyAspMet[redacted]snLysLeuPheAlaGlyIleArgArgAsp

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG  2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla   880

AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG  2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu   900

CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT  2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal   920

CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG  2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu   940

GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC  2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe   960

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG  2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu   980

AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC  3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn  1000

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA  3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro  1020

TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC  3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls  1040

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC  3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly  1060

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC  3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu  1080

AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG  3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln  1100

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC  3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn  1120

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC                          3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp                          1132
```

FIG. 11Q

[redacted]runcated protein 3 (ver.[redacted]

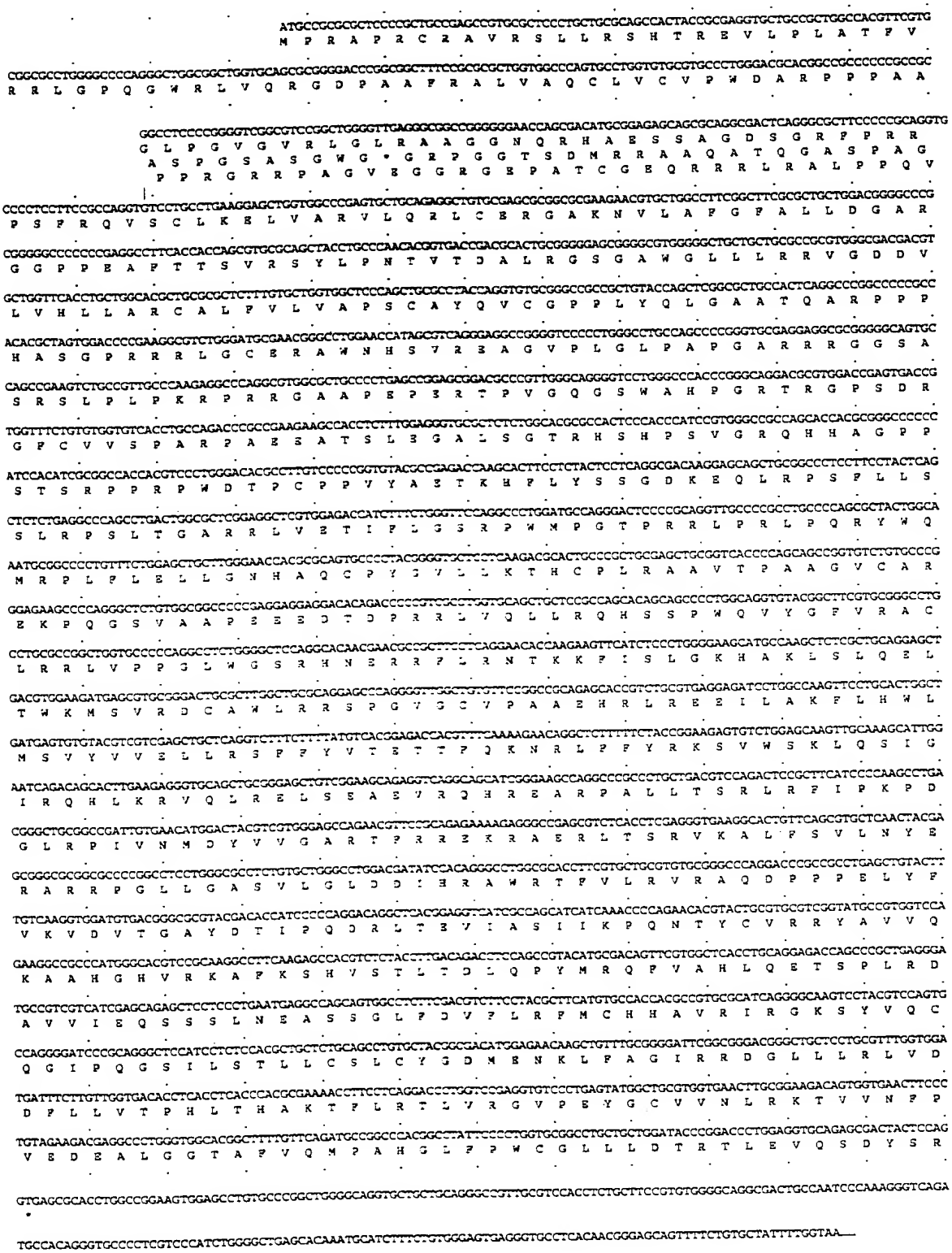


FIG. 11R

[redacted]red C-terminus protein ([redacted] 2)

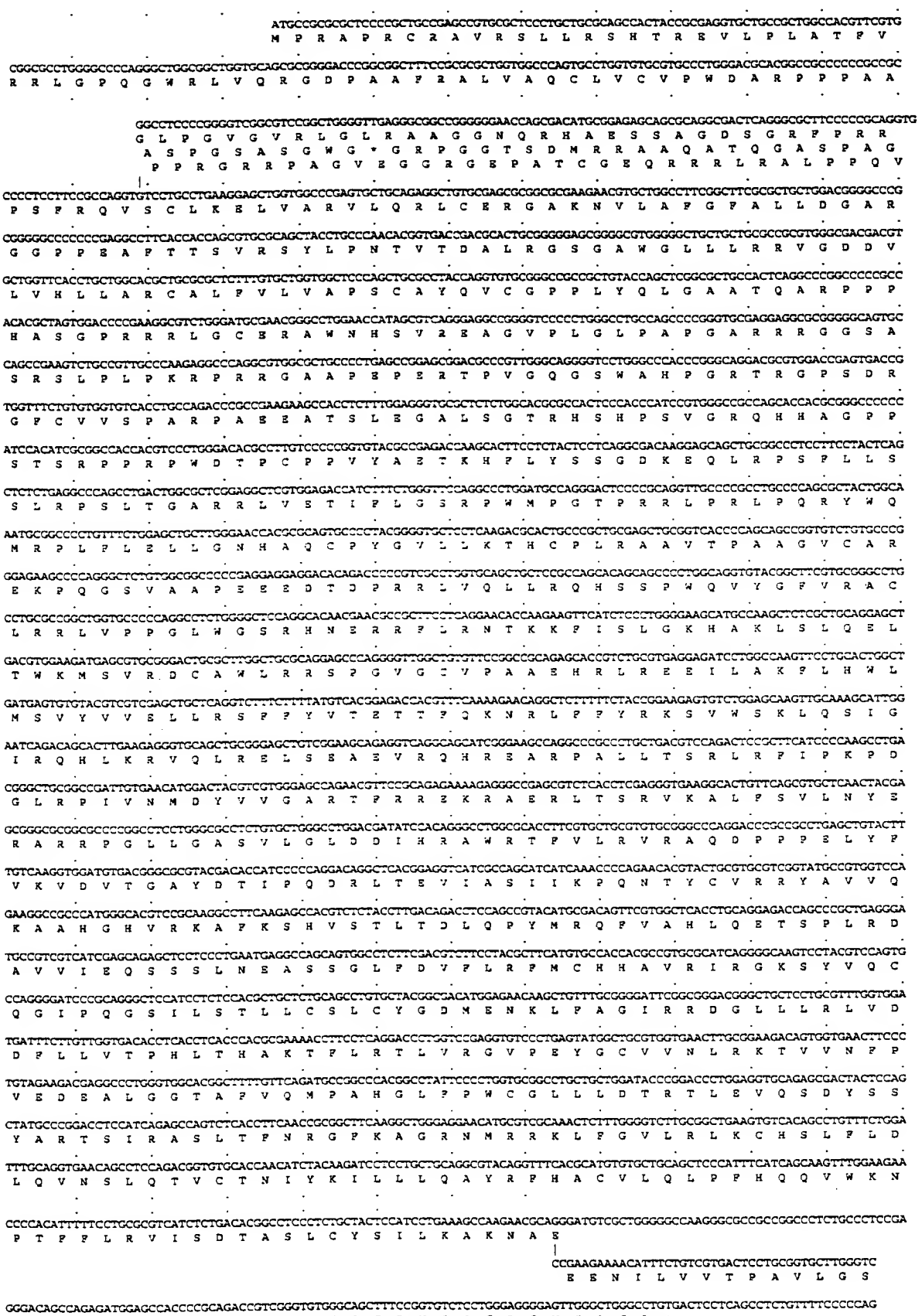


FIG. 11S

Protein that lacks motif A (variant 2)

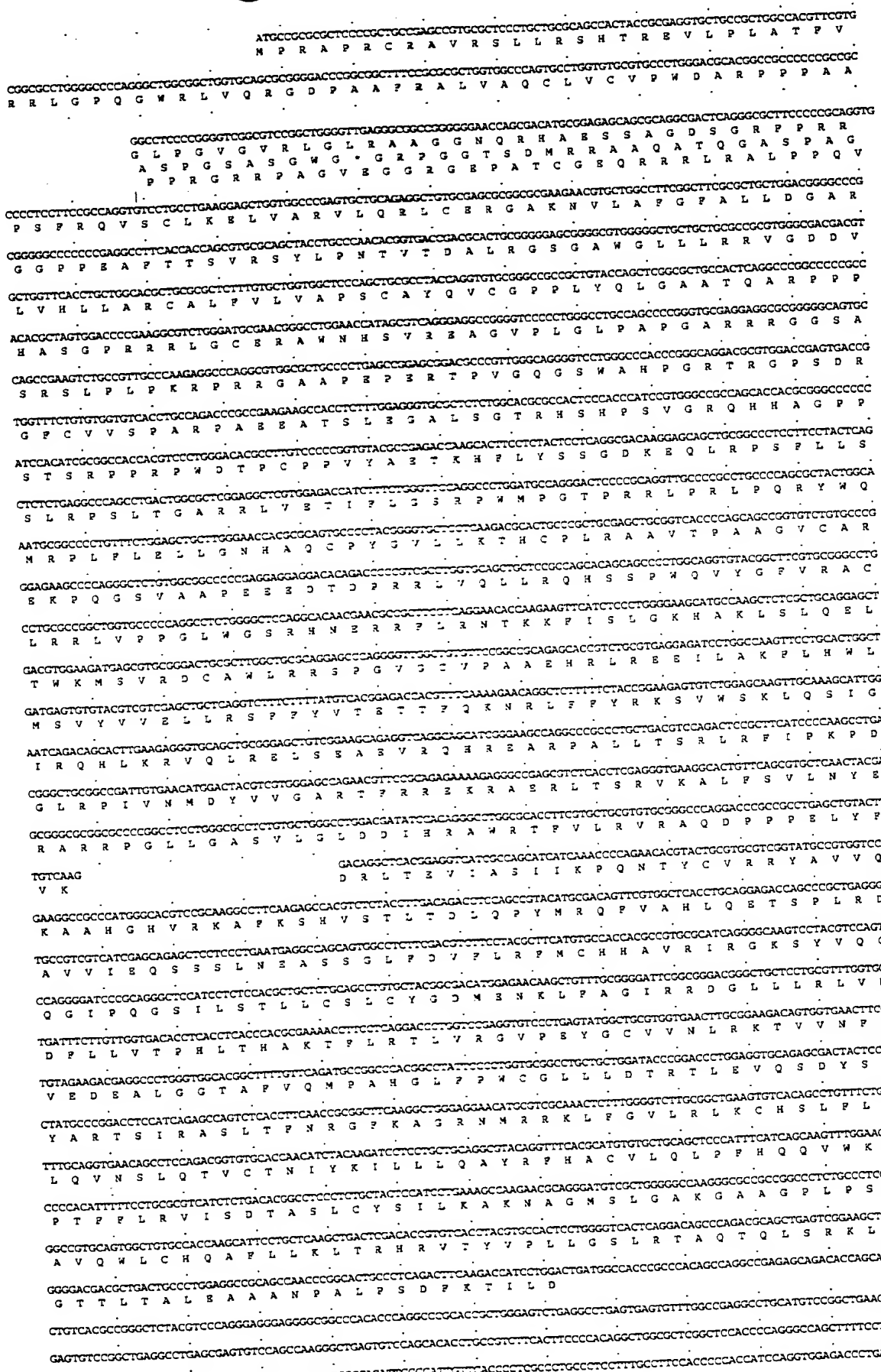


FIG. 11T

GGACCCTGGGAGCTCTGGGAATTTGGAGTGAC[redacted]TGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGT[redacted]AATTGGGGGGAGGTGCTGTGGGAGTAA

AATACTGAATATATGAGTTTTTCAGTTTTGA

FIG. 11U

Trunca[redacted] protein that lacks moti[redacted] (ver. 2)

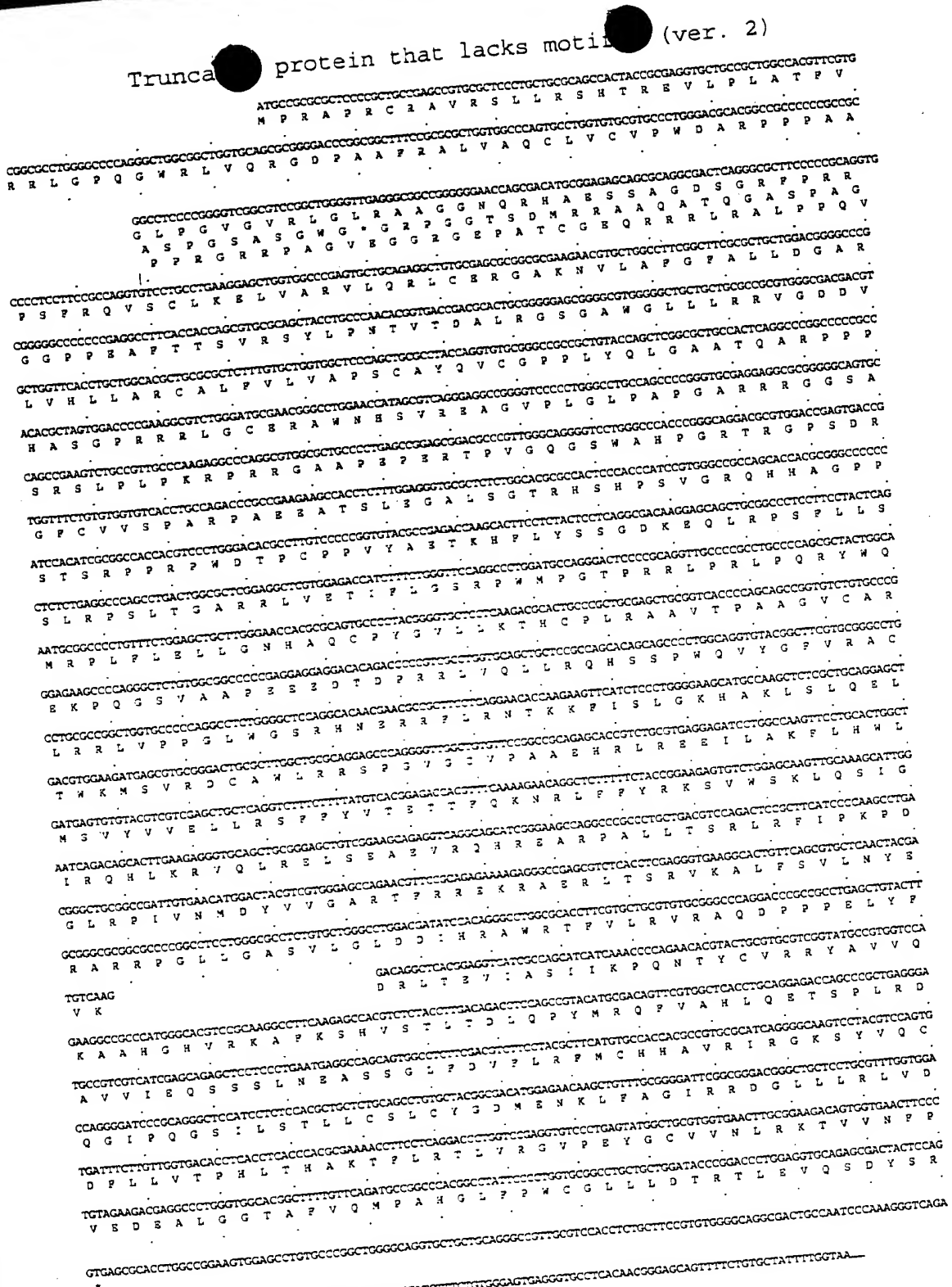


FIG. 11V

Lacks [illegible]if A and altered C-termi[illegible] (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H T R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

TGTCAAG
V K

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
P T F F L R V I S D T A S L C Y S I L K A K N A E

CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC
E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L *

FIG. 11W

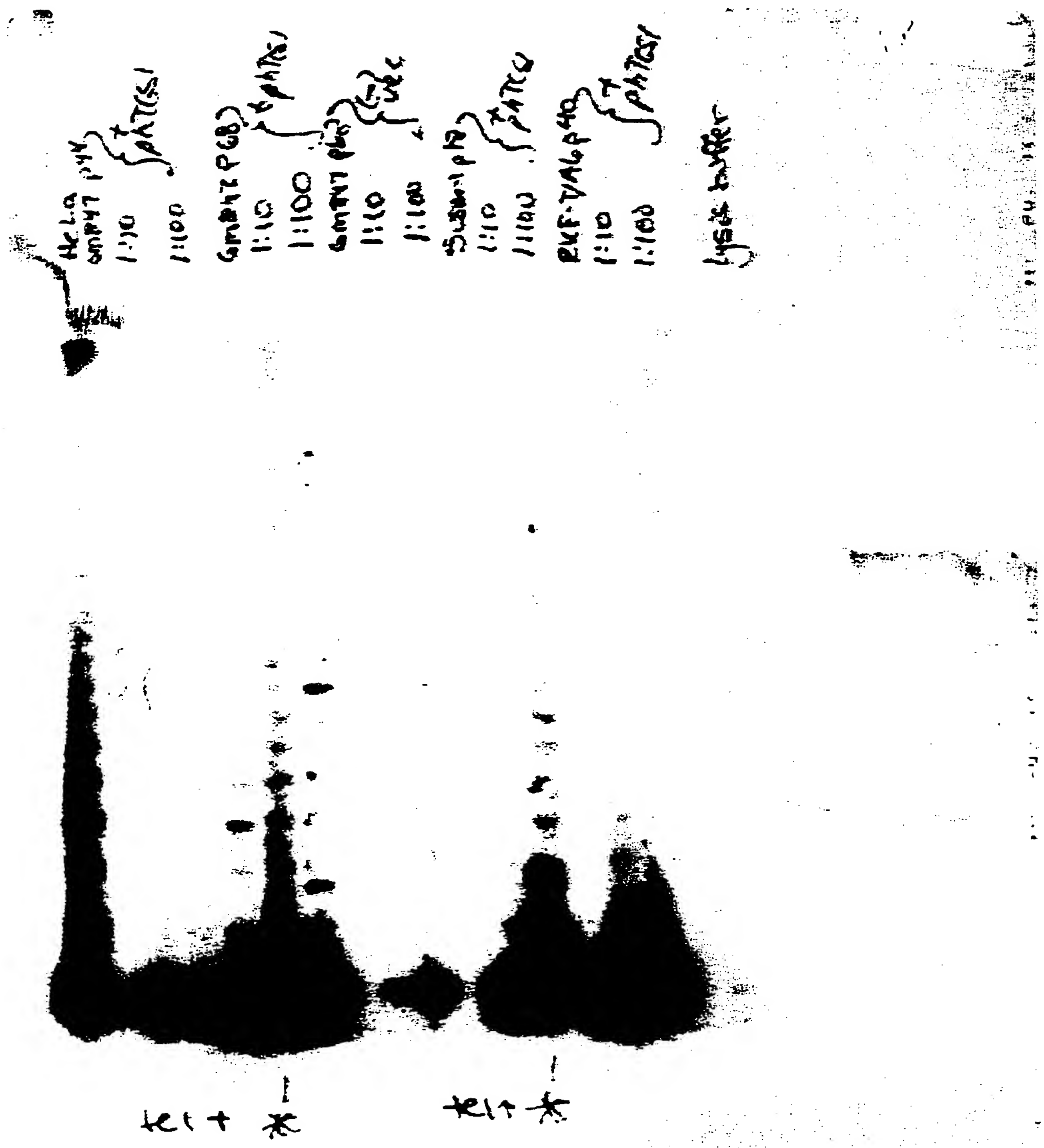


FIG. 12

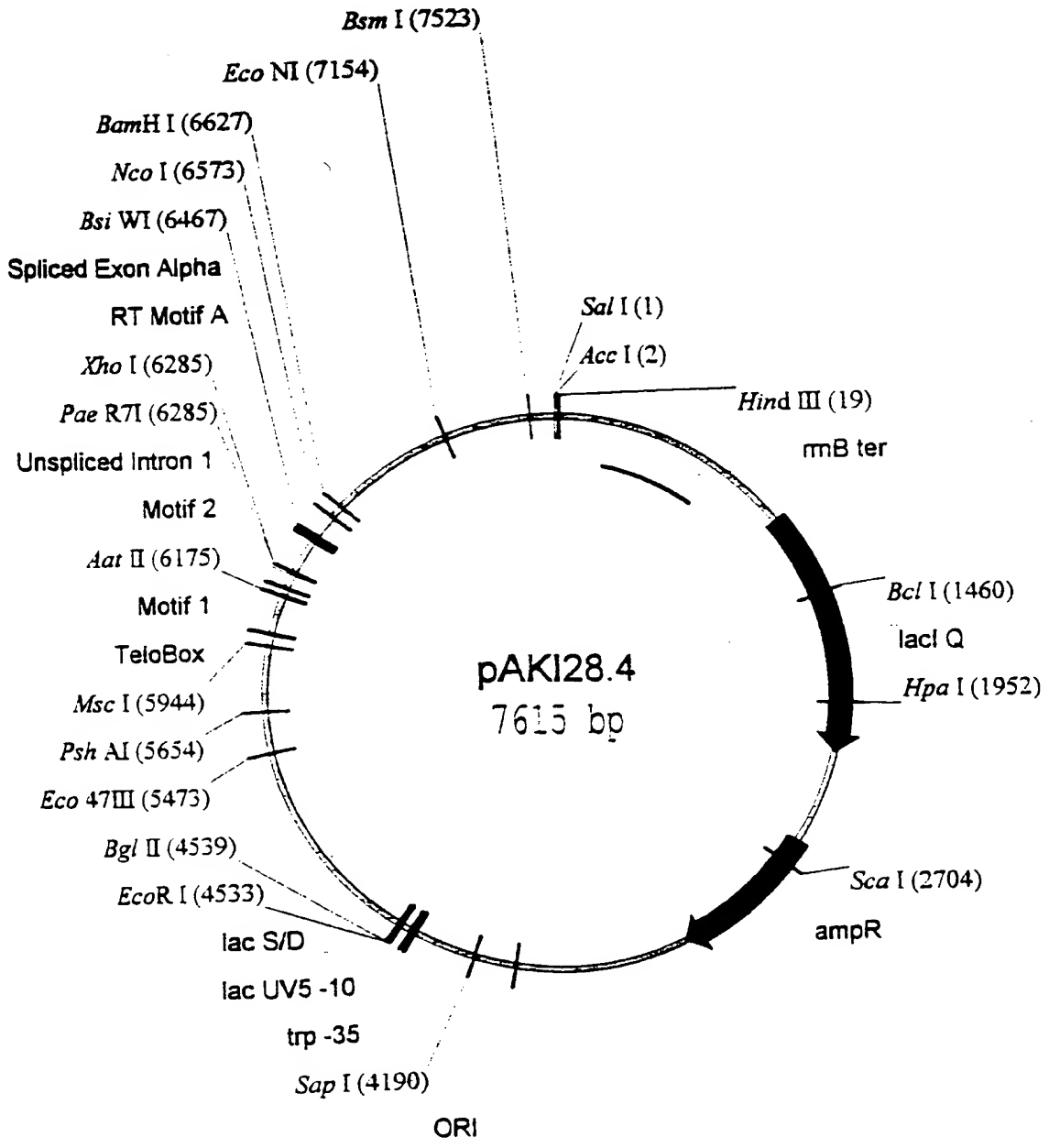

Bsm I (7523)
Eco NI (7154)
BamH I (6627)
Nco I (6573)
Bsi WI (6467)
Spliced Exon Alpha
RT Motif A
Xho I (6285)
Pae R7I (6285)
Unspliced Intron 1
Motif 2
Aat II (6175)
Motif 1
TeloBox
Msc I (5944)
Psh AI (5654)
Eco 47III (5473)
Bgl II (4539)
EcoR I (4533)
lac S/D
lac UV5 -10
trp -35
Sap I (4190)
ORI
Sal I (1)
Acc I (2)
Hind III (19)
rrnB ter
Bcl I (1460)
lacI Q
Hpa I (1952)
Sca I (2704)
ampR
pAKI28.4
7615 bp

FIG. 13A

LOCUS pAKI28.4 7615 bp dsDNA Circular
DEFINITION Human telomerase clone with exon beta spliced out

```
   1 tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa
  61 aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccctttcgc cagctggcgt
 121 aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
 181 tggcgcctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat
 241 tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag
 301 aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc
 361 catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc
 421 gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct
 481 ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag
 541 cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgccataaa
 601 ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggccttttt gcgtttctac
 661 aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc
 721 gtttttgcat caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg
 781 ccgcatagtt aagccagccc cgacacccgc caacacccgc tgacgcgccc tgacgggctt
```

FIG. 13B

```
 841 gtctgctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc
 901 agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat
 961 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca
1021 ccatcgaatg gtgcaaaacc tttcgcggta tggcatgata gcgcccggaa gagagtcaat
1081 tcagggtggt gaatgtgaaa ccagtaacgt tatacgatgt cgcagagtat gccggtgtct
1141 cttatcagac cgtttcccgc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg
1201 aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac
1261 tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc
1321 cgtcgcaaat tgtcgcggcg attaaatctc gcgccgatca actgggtgcc agcgtggtgg
1381 tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaagc ggcggtgcac aatcttctcg
1441 cgcaacgcgt cagtgggctg atcattaact atccgctgga tgaccaggat gccattgctg
1501 tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacaccca
1561 tcaacagtat tattttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg
1621 cattgggtca ccagcaaatc gcgctgttag cgggcccatt aagttctgtc tcggcgcgtc
1681 tgcgtctggc tggctggcat aaatatctca ctcgcaatca aattcagccg atagcggaac
1741 gggaaggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg
1801 gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg
1861 ccattaccga gtccgggctg cgcgttggtg cggatatctc ggtagtggga tacgacgata
1921 ccgaagacag ctcatgttat atcccgccgt taaccaccat caaacaggat tttcgcctgc
1981 tggggcaaac cagcgtggac cgcttgctgc aactctctca gggccaggcg gtgaagggca
2041 atcagctgtt gcccgtctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa
2101 ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac
2161 tggaaagcgg gcagtgagcg caacgcaatt aatgtaagtt agctcactca ttaggcaccc
2221 caggctttac actttatgct tccgacctgc aagaacctca cgtcaggtgg cacttttcgg
2281 ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg
2341 ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt
2401 attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt
2461 gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg
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2581 aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgta
2641 ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg
2701 agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca
2761 gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag
2821 gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact cgccttgatc
2881 gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg
2941 tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact ctagcttccc
3001 ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt ctgcgctcgg
3061 cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt gggtctcgcg
3121 gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt atctacacga
3181 cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac
3241 tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag attgatttaa
3301 aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca
3361 aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag
3421 gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac
3481 cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt ccgaaggtaa
3541 ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg tagttaggcc
3601 accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaatc ctgttaccag
3661 tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac
3721 cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc agcttggagc
3781 gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc
3841 ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca ggagagcgca
3901 cgagggagct tccagggggа aacgcctggt atctttatag tcctgtcggg tttcgccacc
3961 tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta tggaaaaacg
4021 ccagcaacgc ggcctttttа cggttcctgg ccttttgctg gccttttgct cacatgttct
4081 ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag tgagctgata
4141 ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa gcggaagagc
4201 gcccaatacg caaaccgcct ctccccgcgc gttggccgat tcattaatgc agaattaatt
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FIG. 13C

```
4261 ctcatgtttg acagcttatc atcgactgca cggtgcacca atgcttctgg cgtcaggcag
4321 ccatcggaag ctgtggtatg gctgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc
4381 aaggcgcact cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa
4441 tattctgaaa tgagctgttg acaattaatc atcggctcgt ataatgtgtg gaattgtgag
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4561 tggcccgagt gctgcagagg ctgtgcgagc gcggcgcgaa gaacgtgctg gccttcggct
4621 tcgcgctgct ggacggggcc cgcgggggcc cccccgaggc cttcaccacc agcgtgcgca
4681 gctacctgcc caacacggtg accgacgcac tgcgggggag cggggcgtgg gggctgctgc
4741 tgcgccgcgt gggcgacgac gtgctggttc acctgctggc acgctgcgcg ctctttgtgc
4801 tggtggctcc cagctgcgcc taccaggtgt gcgggccgcc gctgtaccag ctcggcgctg
4861 ccactcaggc ccggcccccg ccacacgcta gtggaccccg aaggcgtctg ggatgcgaac
4921 gggcctggaa ccatagcgtc agggaggccg gggtcccccc gggcctgcca gccccgggtg
4981 cgaggaggcg cgggggcagt gccagccgaa gtctgccgtt gcccaagagg cccaggcgtg
5041 gcgctgcccc tgagccggag cggacgcccg ttgggcaggg gtcctgggcc cacccgggca
5101 ggacgcgtgg accgagtgac cgtggtttct gtgtggtgtc acctgccaga cccgccgaag
5161 aagccacctc tttggagggt gcgctcttcg gcacgcgcca ctcccaccca tccgtgggcc
5221 gccagcacca cgcgggcccc ccatccacat cgcggccacc acgtccctgg gacacgcctt
5281 gtcccccggt gtacgccgag accaagcact tcctctactc ctcaggcgac aaggagcagc
5341 tgcggccctc cttcctactc agctcttcga ggcccagcct gactggcgct cggaggctcg
5401 tggagaccat ctttctgggt tccaggcccc ggatgccagg gactccccgc aggttgcccc
5461 gcctgcccca gcgctactgg caaatgcggc ccctgtttct ggagctgctt gggaaccacg
5521 cgcagtgccc ctacggggtg ctcctcaaga cgcactgccc gctgcgagct gcggtcaccc
5581 cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg
5641 aggacacaga ccccgtcgc ctggtgcagc tgctccgcca gcacagcagc ccctggcagg
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5821 ccaagctctc gctgcaggag ctgacgtgga agatgagcgt gcgggactgc gcttggctgc
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5941 tggccaagtt cctgcactgg ctgatgagtg tgtacgtcgt cgagctgctc aggtctttct
6001 tttatgtcac ggagaccacg tttcaaaaga acaggctctt tttctaccgg aagagtgtct
6061 ggagcaagtt gcaaagcatt ggaatcagac agcacttgaa gagggtgcag ctgcgggagc
6121 tgtcggaagc agaggtcagg cagcatcggg aagccaggcc cgccctgctg acgtccagac
6181 tccgcttcat ccccaagcct gacgggctgc ggccgattgt gaacatggac tacgtcgtgg
6241 gagccagaac gttccgcaga gaaaagaggg ccgagcgtct cacctcgagg gtgaaggcac
6301 tgttcagcgt gctcaactac gagcgggcgc ggcgccccgg cctcctgggc gcctctgtgc
6361 tgggcctgga cgatatccac agggcctggc gcaccttcgt gctgcgtgtg cgggcccagg
6421 acccgccgcc tgagctgtac tttgtcaagg tggatgtgac gggcgcgtac gacaccatcc
6481 cccaggacag gctcacggag gtcatcgcca gcatcatcaa accccagaac acgtactgcg
6541 tgcgtcggta tgccgtggtc cagaaggccg cccatgggca cgtccgcaag gccttcaaga
6601 gccacgtcct acgtccagtg ccaggggatc ccgcagggct ccatcctctc cacgctgctc
6661 tgcagcctgt gctacggcga catggagaac aagctgtttg cggggattcg gcgggacggg
6721 ctgctcctgc gtttggtgga tgatttcttg ttggtgacac ctcacctcac ccacgcgaaa
6781 acttcctcag gacctggtcc gaagtgtcct gagtatggct gcgtggtgaa cttgcggaag
6841 acagtggtga acttccctgt agaagacgaa gccctgggtg gcacggcttt tgttcagatg
6901 ccggcccacg gcctattccc ctggtgcggc ctgctgctgg ataccccgac cctggaggtg
6961 cagagcgact actccagcta tgcccggacc tccatcagag ccagtctcac cttcaaccgc
7021 ggcttcaagg ctgggaggaa catgcgtcgc aaactctttg gggtcttgcg gctgaagtgt
7081 cacagcctgt ttctggattt gcaggtgaac agcctccaga cggtgtgcac caacatctac
7141 aagatcctcc tgctgcaggc gtacaggttt cacgcatgtg tgctgcagct cccatttcat
7201 cagcaagttt ggaagaaccc cacatttttc ctgcgcgtca tctctgacac ggcctccctc
7261 tgctactcca tcctgaaagc caagaacgca gccgaagaaa acatttctgt cgtgactcct
7321 gcggtgcttg ggtcgggaca gccagagatg gagccacccc gcagaccgtc gggtgtgggc
7381 agctttccgg tgtctcctgg gaggggagtt gggctgggcc tgtgactcct cagcctctgt
7441 tttccccccag ggatgtcgct gggggccaag ggcgccgccg gccctctgcc ctccgaggcc
7501 gtgcagtggc tgtgccacca agcattcctg ctcaagctga ctcgacaccg tgtcacctac
7561 gtgccactcc tggggtcact caggacaggc aagtgtgggt ggaggccagt gcggg
```

D:\Vector NTI\pAKI28.4.gb

FIG. 13D

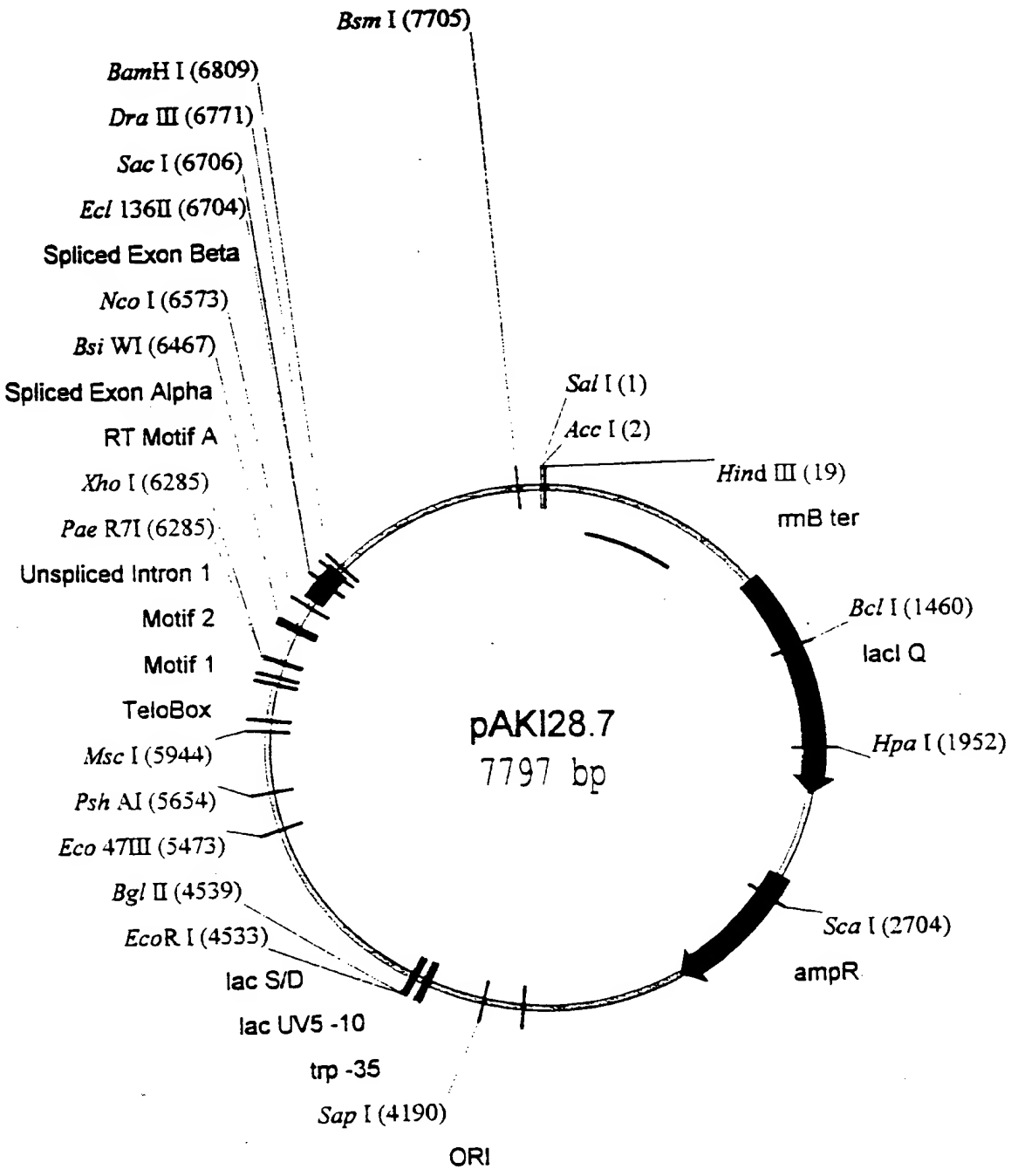
Bsm I (7705)
BamH I (6809)
Dra III (6771)
Sac I (6706)
Ecl 136II (6704)
Spliced Exon Beta
Nco I (6573)
Bsi WI (6467)
Spliced Exon Alpha
RT Motif A
Xho I (6285)
Pae R7I (6285)
Unspliced Intron 1
Motif 2
Motif 1
TeloBox
Msc I (5944)
Psh AI (5654)
Eco 47III (5473)
Bgl II (4539)
EcoR I (4533)
lac S/D
lac UV5 -10
trp -35
Sap I (4190)
ORI
Sal I (1)
Acc I (2)
Hind III (19)
rrnB ter
Bcl I (1460)
lacI Q
Hpa I (1952)
Sca I (2704)
ampR
pAKI28.7
7797 bp

FIG. 14A

LOCUS pAKI28.7 7797 bp dsDNA Circular
DEFINITION Human telomerase clone with alternative C-terminus

```
  1 tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa
 61 aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttcgc cagctggcgt
121 aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
181 tggcgcctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat
241 tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag
301 aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc
361 catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc
421 gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct
481 ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag
```

FIG. 14B

```
 541 cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgccataaa
 601 ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggccttttt gcgtttctac
 661 aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc
 721 gtttttgcat caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg
 781 ccgcatagtt aagccagccc cgacacccgc caacacccgc tgacgcgccc tgacgggctt
 841 gtctgctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc
 901 agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat
 961 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca
1021 ccatcgaatg gtgcaaaacc tttcgcggta tggcatgata gcgcccggaa gagagtcaat
1081 tcagggtggt gaatgtgaaa ccagtaacgt tatacgatgt cgcagagtat gccggtgtct
1141 cttatcagac cgtttcccgc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg
1201 aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac
1261 tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc
1321 cgtcgcaaat tgtcgcggcg attaaatctc gcgccgatca actgggtgcc agcgtggtgg
1381 tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaagc ggcggtgcac aatcttctcg
1441 cgcaacgcgt cagtgggctg atcattaact atccgctgga tgaccaggat gccattgctg
1501 tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacaccca
1561 tcaacagtat tattttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg
1621 cattgggtca ccagcaaatc gcgctgttag cgggcccatt aagttctgtc tcggcgcgtc
1681 tgcgtctggc tggctggcat aaatatctca ctcgcaatca aattcagccg atagcggaac
1741 gggaaggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg
1801 gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg
1861 ccattaccga gtccgggctg cgcgttggtg cggatatctc ggtagtggga tacgacgata
1921 ccgaagacag ctcatgttat atcccgccgt taaccaccat caaacaggat tttcgcctgc
1981 tggggcaaac cagcgtggac cgcttgctgc aactctctca gggccaggcg gtgaagggca
2041 atcagctgtt gcccgtctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa
2101 ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac
2161 tggaaagcgg gcagtgagcg caacgcaatt aatgtaagtt agctcactca ttaggcaccc
2221 caggctttac actttatgct tccgacctgc aagaacctca cgtcaggtgg cacttttcgg
2281 ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg
2341 ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt
2401 attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt
2461 gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg
2521 ggttacatcg agaactggat ctcaacagcg gtaagatcct tgagagtttt cgccccgaag
2581 aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgta
2641 ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg
2701 agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca
2761 gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag
2821 gaccgaagga gctaaccgct tttttgcaca acatgggggga tcatgtaact cgccttgatc
2881 gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg
2941 tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact ctagcttccc
3001 ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt ctgcgctcgg
3061 cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt gggtctcgcg
3121 gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt atctacacga
3181 cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac
3241 tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag attgatttaa
3301 aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca
3361 aaatcccttа acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag
3421 gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac
3481 cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt ccgaaggtaa
3541 ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg tagttaggcc
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3661 tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac
3721 cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc agcttggagc
3781 gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc
3841 ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca ggagagcgca
3901 cgagggagct tccagggga aacgcctggt atctttatag tcctgtcggg tttcgccacc
```

FIG. 14C

```
3961 tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta tggaaaaacg
4021 ccagcaacgc ggccttttta cggttcctgg ccttttgctg gccttttgct cacatgttct
4081 ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag tgagctgata
4141 ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa gcggaagagc
4201 gcccaatacg caaaccgcct ctccccgcgc gttggccgat tcattaatgc agaattaatt
4261 ctcatgtttg acagcttatc atcgactgca cggtgcacca atgcttctgg cgtcaggcag
4321 ccatcggaag ctgtggtatg gctgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc
4381 aaggcgcact cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa
4441 tattctgaaa tgagctgttg acaattaatc atcggctcgt ataatgtgtg gaattgtgag
4501 cggataacaa tttcacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg
4561 tggcccgagt gctgcagagg ctgtgcgagc gcggcgcgaa gaacgtgctg gccttcggct
4621 tcgcgctgct ggacggggcc cgcgggggcc cccccgaggc cttcaccacc agcgtgcgca
4681 gctacctgcc caacacggtg accgacgcac tgcgggggag cggggcgtgg gggctgctgc
4741 tgcgccgcgt gggcgacgac gtgctggttc acctgctggc acgctgcgcg ctctttgtgc
4801 tggtggctcc cagctgcgcc taccaggtgt gcgggccgcc gctgtaccag ctcggcgctg
4861 ccactcaggc ccggcccccg ccacacgcta gtggaccccg aaggcgtctg ggatgcgaac
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5101 ggacgcgtgg accgagtgac cgtggttttt gtgtggtgtc acctgccaga cccgccgaag
5161 aagccacctc tttggagggt gcgctttttg gcacgcgcca ctcccaccca tccgtgggcc
5221 gccagcacca cgcgggcccc ccatccacat cgcggccacc acgtccctgg gacacgcctt
5281 gtcccccggt gtacgccgag accaagcact tcctctactc ctcaggcgac aaggagcagc
5341 tgcggccctc cttcctactc agctctttga ggcccagcct gactggcgct cggaggctcg
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5581 cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg
5641 aggacacaga ccccgtcgc ctggtgcagc tgctccgcca gcacagcagc ccctggcagg
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6061 ggagcaagtt gcaaagcatt ggaatcagac agcacttgaa gagggtgcag ctgcgggagc
6121 tgtcggaagc agaggtcagg cagcatcggg aagccaggcc cgccctgctg acgtccagac
6181 tccgcttcat ccccaagcct gacgggctgc ggccgattgt gaacatggac tacgtcgtgg
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6361 tgggcctgga cgatatccac agggcctggc gcaccttcgt gctgcgtgtg cgggcccagg
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6601 gccacgtctc taccttgaca gacctccagc cgtacatgcg acagttcgtg gctcacctgc
6661 aggagaccag cccgctgagg gatgccgtcg tcatcgagca gagctcctcc ctgaatgagg
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7021 agacagtggt gaacttccct gtagaagacg aagccctggg tggcacggct tttgttcaga
7081 tgccggccca cggcctattc ccctggtgcg gcctgctgct ggatacccgg accctggagg
7141 tgcagagcga ctactccagc tatgcccgga cctccatcag agccagtctc accttcaacc
7201 gcggcttcaa ggctgggagg aacatgcgtc gcaaactctt tggggtcttg cggctgaagt
7261 gtcacagcct gtttctggat ttgcaggtga acagcctcca gacggtgtgc accaacatct
7321 acaagatcct cctgctgcag gcgtacaggt ttcacgcatg tgtgctgcag ctcccatttc
```

FIG. 14D

```
7381 atcagcaagt ttggaagaac cccacatttt tcctgcgcgt catctctgac acggcctccc
7441 tctgctactc catcctgaaa gccaagaacg cagccgaaga aaacatttct gtcgtgactc
7501 ctgcggtgct tgggtcggga cagccagaga tggagccacc ccgcagaccg tcgggtgtgg
7561 gcagctttcc ggtgtctcct gggaggggag ttgggctggg cctgtgactc ctcagcctct
7621 gttttccccc agggatgtcg ctgggggcca agggcgccgc cggccctctg ccctccgagg
7681 ccgtgcagtg gctgtgccac caagcattcc tgctcaagct gactcgacac cgtgtcacct
7741 acgtgccact cctggggtca ctcaggacag gcaagtgtgg gtggaggcca gtgcggg
```

FIG. 14E

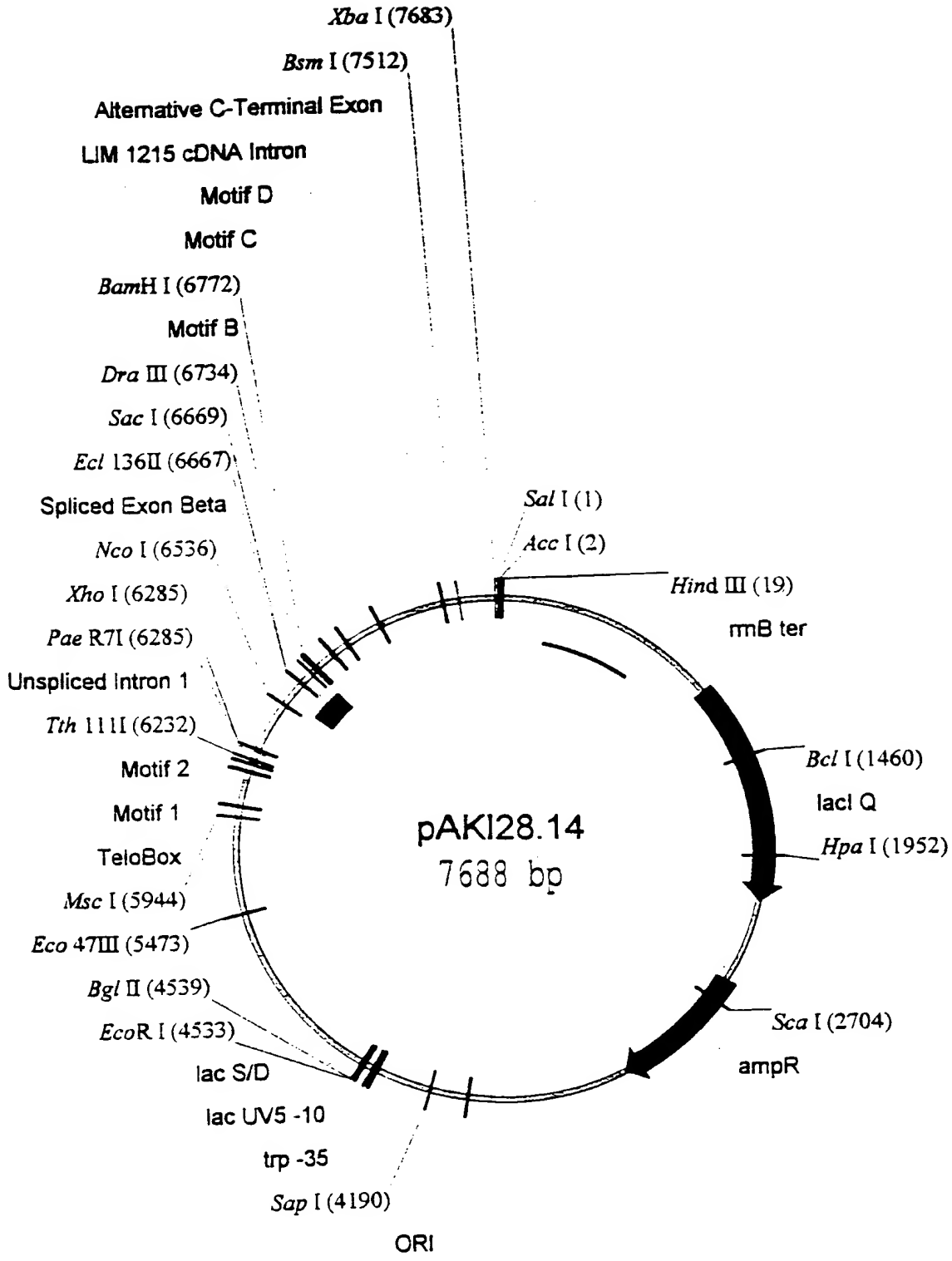
Xba I (7683)
Bsm I (7512)
Alternative C-Terminal Exon
LIM 1215 cDNA Intron
Motif D
Motif C
BamH I (6772)
Motif B
Dra III (6734)
Sac I (6669)
Ecl 136II (6667)
Spliced Exon Beta
Nco I (6536)
Xho I (6285)
Pae R7I (6285)
Unspliced Intron 1
Tth 111I (6232)
Motif 2
Motif 1
TeloBox
Msc I (5944)
Eco 47III (5473)
Bgl II (4539)
EcoR I (4533)
lac S/D
lac UV5 -10
trp -35
Sap I (4190)
ORI
Sal I (1)
Acc I (2)
Hind III (19)
rrnB ter
Bcl I (1460)
lacI Q
Hpa I (1952)
Sca I (2704)
ampR
pAKI28.14
7688 bp

FIG. 15A

LOCUS pAKI28.14 7688 bp dsDNA Circular
DEFINITION Human telomerase clone with exon alpha spliced out

```
   1 tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa
  61 aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttcgcc agctggcgt
 121 aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
 181 tggcgcctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat
 241 tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag
 301 aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc
 361 catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc
 421 gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct
 481 ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag
 541 cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgccataaa
 601 ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggccttttt gcgtttctac
 661 aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc
 721 gtttttgcat caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg
 781 ccgcatagtt aagccagccc cgacacccgc caacacccgc tgacgcgccc tgacgggctt
 841 gtctgctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc
 901 agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat
 961 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca
1021 ccatcgaatg gtgcaaaacc tttcgcggta tggcatgata gcgcccggaa gagagtcaat
1081 tcagggtggt gaatgtgaaa ccagtaacgt tatacgatgt cgcagagtat gccggtgtct
1141 cttatcagac cgtttcccgc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg
1201 aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac
1261 tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc
1321 cgtcgcaaat tgtcgcggcg attaaatctc gcgccgatca actgggtgcc agcgtggtgg
1381 tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaagc ggcggtgcac aatcttctcg
1441 cgcaacgcgt cagtgggctg atcattaact atccgctgga tgaccaggat gccattgctg
1501 tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacaccca
1561 tcaacagtat tattttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg
1621 cattgggtca ccagcaaatc gcgctgttag cgggcccatt aagttctgtc tcggcgcgtc
1681 tgcgtctggc tggctggcat aaatatctca ctcgcaatca aattcagccg atagcggaac
1741 gggaaggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg
1801 gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg
1861 ccattaccga gtccgggctg cgcgttggtg cggatatctc ggtagtggga tacgacgata
1921 ccgaagacag ctcatgttat atcccgccgt taaccaccat caaacaggat tttcgcctgc
1981 tggggcaaac cagcgtggac cgcttgctgc aactctctca gggccaggcg gtgaagggca
2041 atcagctgtt gcccgtctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa
2101 ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac
2161 tggaaagcgg gcagtgagcg caacgcaatt aatgtaagtt agctcactca ttaggcaccc
2221 caggctttac actttatgct tccgacctgc aagaacctca cgtcaggtgg cacttttcgg
2281 ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg
2341 ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt
2401 attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt
2461 gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg
2521 ggttacatcg agaactggat ctcaacagcg gtaagatcct tgagagtttt cgccccgaag
2581 aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgta
2641 ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg
2701 agtactcacc agtcacagaa aagcatcttа cggatggcat gacagtaaga gaattatgca
2761 gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag
2821 gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact cgccttgatc
2881 gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg
2941 tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact ctagcttccc
3001 ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt ctgcgctcgg
3061 cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt gggtctcgcg
3121 gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt atctacacga
3181 cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac
3241 tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag attgatttaa
3301 aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca
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FIG. 15B

3361 aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag
3421 gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac
3481 cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt ccgaaggtaa
3541 ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg tagttaggcc
3601 accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaatc ctgttaccag
3661 tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac
3721 cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc agcttggagc
3781 gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc
3841 ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca ggagagcgca
3901 cgagggagct tccaggggga aacgcctggt atctttatag tcctgtcggg tttcgccacc
3961 tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta tggaaaaacg
4021 ccagcaacgc ggccttttta cggttcctgg ccttttgctg gccttttgct cacatgttct
4081 ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag tgagctgata
4141 ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa gcggaagagc
4201 gcccaatacg caaaccgcct ctccccgcgc gttggccgat tcattaatgc agaattaatt
4261 ctcatgtttg acagcttatc atcgactgca cggtgcacca atgcttctgg cgtcaggcag
4321 ccatcggaag ctgtggtatg gctgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc
4381 aaggcgcact cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa
4441 tattctgaaa tgagctgttg acaattaatc atcggctcgt ataatgtgtg gaattgtgag
4501 cggataacaa tttcacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg
4561 tggcccgagt gctgcagagg ctgtgcgagc gcggcgcgaa gaacgtgctg gccttcggct
4621 tcgcgctgct ggacggggcc cgcgggggcc cccccgaggc cttcaccacc agcgtgcgca
4681 gctacctgcc caacacggtg accgacgcac tgcgggggag cggggcgtgg gggctgctgc
4741 tgcgccgcgt gggcgacgac gtgctggttc acctgctggc acgctgcgcg ctctttgtgc
4801 tggtggctcc cagctgcgcc taccaggtgt gcgggccgcc gctgtaccag ctcggcgctg
4861 ccactcaggc ccggcccccg ccacacgcta gtggaccccg aaggcgtctg ggatgcgaac
4921 gggcctggaa ccatagcgtc agggaggccg gggtccccct gggcctgcca gccccgggtg
4981 cgaggaggcg cgggggcagt gccagccgaa gtctgccgtt gcccaagagg cccaggcgtg
5041 gcgctgcccc tgagccggag cggacgcccg ttgggcaggg gtcctgggcc cacccgggca
5101 ggacgcgtgg accgagtgac cgtggtttct gtgtggtgtc acctgccaga cccgccgaag
5161 aagccacctc tttggagggt gcgctctctg gcacgcgcca ctcccaccca tccgtgggcc
5221 gccagcacca cgcgggcccc ccatccacat cgcggccacc acgtccctgg gacacgcctt
5281 gtcccccggt gtacgccgag accaagcact tcctctactc ctcaggcgac aaggagcagc
5341 tgcggccctc cttcctactc agctctctga ggcccagcct gactggcgct cggaggctcg
5401 tggagaccat ctttctgggt tccaggccct ggatgccagg gactccccgc aggttgcccc
5461 gcctgcccca gcgctactgg caaatgcggc ccctgtttct ggagctgctt gggaaccacg
5521 cgcagtgccc ctacggggtg ctcctcaaga cgcactgccc gctgcgagct gcggtcaccc
5581 cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg
5641 aggacacaga cccccgtcgc ctggtgcagc tgctccgcca gcacagcagc ccctggcagg
5701 tgtacggctt cgtgcgggcc tgcctgcgcc ggctggtgcc cccaggcctc tggggctcca
5761 ggcacaacga acgccgcttc ctcaggaaca ccaagaagtt catctccctg gggaagcatg
5821 ccaagctctc gctgcaggag ctgacgtgga agatgagcgt gcgggactgc gcttggctgc
5881 gcaggagccc aggggttggc tgtgttccgg ccgcagagca ccgtctgcgt gaggagatcc
5941 tggccaagtt cctgcactgg ctgatgagtg tgtacgtcgt cgagctgctc aggtctttct
6001 tttatgtcac ggagaccacg tttcaaaaga acaggctctt tttctaccgg aagagtgtct
6061 ggagcaagtt gcaaagcatt ggaatcagac agcacttgaa gagggtgcag ctgcgggagc
6121 tgtcggaagc agaggtcagg cagcatcggg aagccaggcc cgccctgctg acgtccagac
6181 tccgcttcat ccccaagcct gacgggctgc ggccgattgt gaacatggac tacgtcgtgg
6241 gagccagaac gttccgcaga gaaaagaggg ccgagcgtct cacctcgagg gtgaaggcac
6301 tgttcagcgt gctcaactac gagcgggcgc ggcgccccgg cctcctgggc gcctctgtgc
6361 tgggcctgga cgatatccac agggcctggc gcaccttcgt gctgcgtgtg cgggcccagg
6421 acccgccgcc tgagctgtac tttgtcaagg acaggctcac ggaggtcatc gccagcatca
6481 tcaaacccag aacacgtact gcgtgcgtcg gtatgccgtg gtccagaagg ccgcccatgg
6541 gcacgtccgc aaggccttca agagccacgt ctctaccttg acagacctcc agccgtacat
6601 gcgacagttc gtggctcacc tgcaggagac cagcccgctg agggatgccg tcgtcatcga
6661 gcagagctcc tccctgaatg aggccagcag tggcctcttc gacgtcttcc tacgcttcat
6721 gtgccaccac gccgtgcgca tcaggggcaa gtcctacgtc cagtgccagg ggatcccgca

FIG. 15C

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6781 gggctccatc ctctccacgc tgctctgcag cctgtgctac ggcgacatgg agaacaagct
6841 gtttgcgggg attcggcggg acgggctgct cctgcgtttg gtggatgatt tcttgttggt
6901 gacacctcac ctcacccacg cgaaaacctt cctcaggacc ctggtccgag gtgtccctga
6961 gtatggctgc gtggtgaact tgcggaagac agtggtgaac ttccctgtag aagacgaggc
7021 cctgggtggc acggcttttg ttcagatgcc ggcccacggc ctattccccc ggtgcggcct
7081 gctgctggat acccggaccc tggaggtgca gagcgactac tccagctatg cccggacctc
7141 catcagagcc agtctcacct tcaaccgcgg cttcaaggct gggaggaaca tgcgtcgcaa
7201 actctttggg gtcttgcggc tgaagtgtca cagcctgttt ctggatttgc aggtgaacag
7261 cctccagacg gtgtgcacca acatctacaa gatcctcctg ctgcaggcgt acaggtttca
7321 cgcatgtgtg ctgcagctcc catttcatca gcaagtttgg aagaacccca cattttcct
7381 gcgcgtcatc tctgacacgg cctccctctg ctactccatc ctgaaagcca agaacgcagg
7441 gatgtcgctg ggggccaagg gcgccgccgg ccctctgccc tccgaggccg tgcagtggct
7501 gtgccaccaa gcattcctgc tcaagctgac tcgacaccgt gtcacctacg tgccactcct
7561 ggggtcactc aggacagccc agacgcagct gagtcggaag ctcccgggga cgacgctgac
7621 tgccctggag gccgcagcca acccggcact gccctcagac ttcaagacca tcctggactg
7681 atctagag
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FIG. 15D